

BLAST analysis SARS-Cov-2 against Streptococcus Pneumoniae

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3.1.550 NC_045512.2 SARS-Cov-2 27309-27326:	207
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3.1.554 NC_045512.2 SARS-Cov-2 15972-15987:	208
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3.1.557 NC_045512.2 SARS-Cov-2 17086-17100:	209
3.1.558 NC_045512.2 SARS-Cov-2 10737-10756:	209
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3.1.560 NC_045512.2 SARS-Cov-2 3851-3865:	210
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3.1.562 NC_045512.2 SARS-Cov-2 3029-3049:	211
3.1.563 NC_045512.2 SARS-Cov-2 13681-13701:	211
3.1.564 NC_045512.2 SARS-Cov-2 3804-3818:	211
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3.1.571 NC_045512.2 SARS-Cov-2 16603-16641:	213
3.1.572 NC_045512.2 SARS-Cov-2 26086-26104:	214
3.1.573 NC_045512.2 SARS-Cov-2 22890-22909:	214
3.1.574 NC_045512.2 SARS-Cov-2 4740-4754:	214
3.1.575 NC_045512.2 SARS-Cov-2 11174-11188:	215
3.1.576 NC_045512.2 SARS-Cov-2 17436-17450:	215

1 Introduction

The study was performed by `blastn` analysis with SARS-Cov-2 against *Streptococcus pneumoniae* H17 genomic sequences. Considering there is no hitting when blast analysis with whole length of SARS-Cov-2, we spliced the SARS-Cov-2 virus genome sequence into segments of 1,000bp with sliding windows of 50bp, and then conducted blast analysis on these segments against sequences of *Streptococcus pneumoniae*.

2 Methods

2.1 SARS-Cov-2 genome sequence splicing

The genome sequence of SARS-Cov-2 virus were spliced into segments of 1,000bp length, with starting positions shifting from 1 to 950 at interval of 50bp. In total 20 sets of segments were created.

2.2 Blast analysis

The 20 sets of SARS-Cov-2 genome segments were compared against sequences of *Streptococcus pneumoniae* downloaded from NCBI (https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/002/076/835/GCF_002076835.1_ASM207683v1/GCF_002076835.1_ASM207683v1_genomic.fna.gz) with `blastn` tools (2.13.0+) on a linux server, respectively.

2.3 Results retrieving and sorting

The hits/alignments on genome of *Streptococcus pneumoniae* reported by the blast analysis were retrieved with customized python scripts. Common hits across different sets of SARS-Cov-2 genome segments were merged.

Table 2: Number of hits by Streptococcus pneumoniae sequences (continued)

Streptococcus pneumoniae	hits
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 15154-15174	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 29306-29325	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 24205-24231	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 7063-7077	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 2236-2250	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 5057-5071	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 17680-17694	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 5592-5610	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 26551-26568	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 23323-23337	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 21951-22005	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 20947-20969	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 29806-29823	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 5279-5299	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 22393-22412	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 21670-21685	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 19743-19762	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 11135-11150	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 3804-3825	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 19561-19575	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 28018-28032	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 14830-14844	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 4333-4359	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 1698-1712	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 19750-19764	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 2110-2128	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 4783-4805	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 29821-29836	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 21464-21487	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 3716-3742	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 17256-17270	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 13094-13113	1
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome Length=2148350 Query = NC_045512.2 SARS-Cov-2 25744-25765	1

3.1 Hits/Alignments

3.1.1 NC_045512.2 SARS-Cov-2 1693-1712:

TTTGGCATCTTTTTCTGCTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1693-1712
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
```

```
Query  943      TTTGGCATCTTTTTCTGCTT  962
      |||| |
Sbjct  241762    TTTGCCATCTTTTTCTCCTT  241743
```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350

Query = NC_045512.2 SARS-Cov-2 1693-1712

Score = 28.3 bits (30), Expect = 6.2

Identities = 18/20 (90%), Gaps = 0/20 (0%)

Strand=Plus/Plus

```
Query  943      TTTGGCATCTTTTTCTGCTT  962
      |||| |
Sbjct  1488055    TTTGTCATCTTTTTCTCCTT  1488074
```

3.1.2 NC_045512.2 SARS-Cov-2 22895-22909:

GTTGGTGGTAATTAT

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350

Query = NC_045512.2 SARS-Cov-2 22895-22909

Score = 28.3 bits (30), Expect = 6.2

Identities = 15/15 (100%), Gaps = 0/15 (0%)

Strand=Plus/Plus

```
Query  145      GTTGGTGGTAATTAT  159
      ||
Sbjct  72168      GTTGGTGGTAATTAT  72182
```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350

Query = NC_045512.2 SARS-Cov-2 22895-22909

Score = 28.3 bits (30), Expect = 6.2

Identities = 15/15 (100%), Gaps = 0/15 (0%)

Strand=Plus/Plus

```
Query  145      GTTGGTGGTAATTAT  159
      ||
Sbjct  543959    GTTGGTGGTAATTAT  543973
```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350

Query = NC_045512.2 SARS-Cov-2 22890-22909

Score = 28.3 bits (30), Expect = 6.2

Identities = 18/20 (90%), Gaps = 0/20 (0%)

```

Strand=Plus/Plus
Query  140      CTAAGGTTGGTGGTAATTAT  159
          |||
Sbjct  830301    CTAAGGTTGGTGAAACTAT  830320

```

3.1.3 NC_045512.2 SARS-Cov-2 4736-4753:

ACTTCTTCTTCTAAAACA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  4736-4753
Score = 29.2 bits (31),  Expect = 6.2
  Identities = 17/18 (94%), Gaps = 0/18 (0%)
  Strand=Plus/Plus
Query  936      ACTTCTTCTTCTAAAACA  953
          |||
Sbjct  649359    ACTTCTACTTCTAAAACA  649376

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  4736-4753
Score = 29.2 bits (31),  Expect = 6.2
  Identities = 17/18 (94%), Gaps = 0/18 (0%)
  Strand=Plus/Minus
Query  936      ACTTCTTCTTCTAAAACA  953
          |||
Sbjct  893275    ACTTCTGCTTCTAAAACA  893258

```

3.1.4 NC_045512.2 SARS-Cov-2 29846-29858:

TTTAATAGCTTCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  29846-29858
Score = 24.7 bits (26),  Expect = 6.3
  Identities = 13/13 (100%), Gaps = 0/13 (0%)
  Strand=Plus/Plus
Query  46      TTTAATAGCTTCT  58
          |||
Sbjct  1202237    TTTAATAGCTTCT  1202249

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350

```

```

Query = NC_045512.2 SARS-Cov-2 29846-29858
Score = 24.7 bits (26), Expect = 6.3
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus
Query 46          TTTAATAGCTTCT 58
          |||
Sbjct 1568441 TTTAATAGCTTCT 1568453

```

3.1.5 NC_045512.2 SARS-Cov-2 3404-3418:

GAAGAAGCTAAAAAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3404-3418
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 654          GAAGAAGCTAAAAAG 668
          |||
Sbjct 159299 GAAGAAGCTAAAAAG 159313

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3404-3418
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 654          GAAGAAGCTAAAAAG 668
          |||
Sbjct 1909636 GAAGAAGCTAAAAAG 1909650

```

3.1.6 NC_045512.2 SARS-Cov-2 13631-13650:

ATTTAATTGATTCTTACTTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13631-13650
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 881          ATTTAATTGATTCTTACTTT 900
          |||
Sbjct 426490 ATTTAATTGATTCTAATTTT 426471

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13631-13650
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 881      ATTTAATTGATTCTTACTTT 900
          ||| |||| |||||
Sbjct 1554249 ATTAAATTTATTCTTACTTT 1554230

```

3.1.7 NC_045512.2 SARS-Cov-2 11985-11999:

CCTTTGAAAAAATGG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11985-11999
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 235      CCTTTGAAAAAATGG 249
          |||||
Sbjct 466315   CCTTTGAAAAAATGG 466301

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11985-11999
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 235      CCTTTGAAAAAATGG 249
          |||||
Sbjct 1969663 CCTTTGAAAAAATGG 1969677

```

3.1.8 NC_045512.2 SARS-Cov-2 29846-29859:

TTTAATAGCTTCTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29846-29859
Score = 26.5 bits (28), Expect = 2.9
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus
Query 96       TTTAATAGCTTCTT 109

```

```
          |||||
Sbjct 1105911 TTTAATAGCTTCTT 1105924
```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350

Query = NC_045512.2 SARS-Cov-2 29846-29859
Score = 26.5 bits (28), Expect = 2.9
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus

```
Query 96          TTTAATAGCTTCTT 109
          |||||
Sbjct 1904579 TTTAATAGCTTCTT 1904592
```

3.1.9 NC_045512.2 SARS-Cov-2 18220-18234:

AAAATGAATTATCAA

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350

Query = NC_045512.2 SARS-Cov-2 18220-18234
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

```
Query 470        AAAATGAATTATCAA 484
          |||||
Sbjct 147277 AAAATGAATTATCAA 147291
```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350

Query = NC_045512.2 SARS-Cov-2 18220-18234
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

```
Query 470        AAAATGAATTATCAA 484
          |||||
Sbjct 1114691 AAAATGAATTATCAA 1114705
```

3.1.10 NC_045512.2 SARS-Cov-2 29810-29822:

GTAAAATTAATTT

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350

Query = NC_045512.2 SARS-Cov-2 29810-29822
Score = 24.7 bits (26), Expect = 6.3

```

Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus
Query  10      GTAAAATTAATTT  22
          |||
Sbjct  274329  GTAAAATTAATTT  274341

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  29810-29822
Score = 24.7 bits (26), Expect = 6.3
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus
Query  10      GTAAAATTAATTT  22
          |||
Sbjct  799517  GTAAAATTAATTT  799529

```

3.1.11 NC_045512.2 SARS-Cov-2 5972-5986:

GACAATTCTTATTTTC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  5972-5986
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query  222      GACAATTCTTATTTTC  236
          |||
Sbjct  1019853  GACAATTCTTATTTTC  1019839

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  5972-5986
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query  222      GACAATTCTTATTTTC  236
          |||
Sbjct  1793645  GACAATTCTTATTTTC  1793659

```

3.1.12 NC_045512.2 SARS-Cov-2 2017-2034:

GATGTTACATCTGATTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome

```

```

Length=2148350
Query = NC_045512.2 SARS-Cov-2 2017-2034
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 267      GATGTTACATCTGATT 284
            |||
Sbjct 263490   GATGTTACATCTTATT 263507

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2017-2034
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 267      GATGTTACATCTGATT 284
            |||
Sbjct 509597   GATGTTACATCTTATT 509580

```

3.1.13 NC_045512.2 SARS-Cov-2 7309-7327:

ATTGTTTTTCAGCTATTTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7309-7327
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Minus
Query 559      ATTGTTTTTCAGCTATTT 577
            |||
Sbjct 929764   ATTCTTTTTTCAGCTATTT 929746

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7309-7327
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Minus
Query 559      ATTGTTTTTCAGCTATTT 577
            |||
Sbjct 930028   ATTCTTTTTTCAGCTATTT 930010

```

3.1.14 NC_045512.2 SARS-Cov-2 29856-29867:

TCTTAGGAGAAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29856-29867
Score = 22.9 bits (24), Expect = 8.9
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus
Query 6          TCTTAGGAGAAT 17
          |||
Sbjct 647621     TCTTAGGAGAAT 647632
```

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29856-29867
Score = 22.9 bits (24), Expect = 8.9
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Plus
Query 6          TCTTAGGAGAAT 17
          |||
Sbjct 959482     TCTTAGGAGAAT 959493
```

3.1.15 NC_045512.2 SARS-Cov-2 1440-1455:

GCTTGAAAACCATTCT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1440-1455
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 690        GCTTGAAAACCATTCT 705
          |||
Sbjct 1967366    GCTTGAAAACCATTCT 1967351
```

3.1.16 NC_045512.2 SARS-Cov-2 25762-25789:

ATAATGAGGCTTTGGCTTTGCTGGAAAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 25762-25789
Score = 29.2 bits (31), Expect = 6.2
```

Identities = 23/28 (82%), Gaps = 0/28 (0%)
 Strand=Plus/Minus
 Query 12 ATAATGAGGCTTTGGCTTTGCTGGAAAT 39
 ||| | |||| | || |||||
 Sbjct 1531207 ATATTCAGGCTCTAGCCTTGCTGGAAAT 1531180

3.1.17 NC_045512.2 SARS-Cov-2 5592-5610:

ATGAACAATTTAAGAAAGG

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 5592-5610
 Score = 31.0 bits (33), Expect = 1.8
 Identities = 18/19 (95%), Gaps = 0/19 (0%)
 Strand=Plus/Plus
 Query 842 ATGAACAATTTAAGAAAGG 860
 ||||| |||||
 Sbjct 369818 ATGAAAAATTTAAGAAAGG 369836

3.1.18 NC_045512.2 SARS-Cov-2 29802-29814:

CCTAATGTGTAAA

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 29802-29814
 Score = 24.7 bits (26), Expect = 6.3
 Identities = 13/13 (100%), Gaps = 0/13 (0%)
 Strand=Plus/Minus
 Query 2 CCTAATGTGTAAA 14
 |||||
 Sbjct 1720579 CCTAATGTGTAAA 1720567

3.1.19 NC_045512.2 SARS-Cov-2 21073-21087:

GTTACAAAAGAAAAT

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 21073-21087
 Score = 28.3 bits (30), Expect = 6.2
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus
 Query 323 GTTACAAAAGAAAAT 337
 |||||
 Sbjct 267789 GTTACAAAAGAAAAT 267803

3.1.20 NC_045512.2 SARS-Cov-2 7915-7929:

AGAATCATCTGCAAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7915-7929
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 165      AGAATCATCTGCAAA 179
          |||
Sbjct 410170   AGAATCATCTGCAAA 410156
```

3.1.21 NC_045512.2 SARS-Cov-2 28969-28983:

CAAAATGTCTGGTAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 28969-28983
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 219      CAAAATGTCTGGTAA 233
          |||
Sbjct 1486124   CAAAATGTCTGGTAA 1486110
```

3.1.22 NC_045512.2 SARS-Cov-2 13564-13578:

GTAGCTGGTTTTGCT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13564-13578
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 814      GTAGCTGGTTTTGCT 828
          |||
Sbjct 624540   GTAGCTGGTTTTGCT 624526
```

3.1.23 NC_045512.2 SARS-Cov-2 2800-2819:

TGATGAAAGGATTGATAAAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2800-2819
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 50      TGATGAAAGGATTGATAAAG 69
          || ||||| |||||
Sbjct 986949  TGTGAAATGATTGATAAAG 986968

```

3.1.24 NC_045512.2 SARS-Cov-2 20867-20881:

TTGGTGCTGGTTCTG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 20867-20881
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 117     TTGGTGCTGGTTCTG 131
          |||||
Sbjct 801235  TTGGTGCTGGTTCTG 801221

```

3.1.25 NC_045512.2 SARS-Cov-2 3940-3959:

AAAACAAGATGATAAGAAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3940-3959
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 190     AAAACAAGATGATAAGAAAA 209
          |||||
Sbjct 818018  AAAACAAGATGCAAAGAAAA 818037

```

3.1.26 NC_045512.2 SARS-Cov-2 1620-1635:

AAATACTCCAAAAAGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1620-1635
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)

```

```

Strand=Plus/Minus
Query  870      AAATACTCCAAAAAGA  885
          |||
Sbjct  1545385  AAATACTCCAAAAAGA  1545370

```

3.1.27 NC_045512.2 SARS-Cov-2 1131-1147:

AAAAGAAAAAGCTTGAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  1131-1147
Score = 31.9 bits (34),  Expect = 0.51
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus
Query  381      AAAAGAAAAAGCTTGAT  397
          |||
Sbjct  1038716  AAAAGAAAAAGCTTGAT  1038732

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  1123-1147
Score = 28.3 bits (30),  Expect = 6.2
Identities = 21/25 (84%), Gaps = 0/25 (0%)
Strand=Plus/Plus
Query  373      AAGGGTTGAAAAGAAAAGCTTGAT  397
          || |||
Sbjct  464789  AACGGTTGAAAAGAGTAACCTTGAT  464813

```

3.1.28 NC_045512.2 SARS-Cov-2 8822-8841:

TTGATTGCTGCAGTCATAAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  8822-8841
Score = 28.3 bits (30),  Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query  72      TTGATTGCTGCAGTCATAAC  91
          |||| | |||
Sbjct  1589447  TTGATCGTTGCAGTCATAAC  1589466

```

3.1.29 NC_045512.2 SARS-Cov-2 26291-26315:

GCGTACTT-CTTTTTCTTGCTTTCGT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 26291-26315
Score = 29.2 bits (31), Expect = 6.2
Identities = 23/27 (85%), Gaps = 2/27 (7%)
Strand=Plus/Minus
Query 541      GCGTACTT--CTTTTTCTTGCTTTCGT 565
          || ||||| ||||| ||||| ||||| ||
Sbjct 1615446 GCTTACTTTGCTTTTTCTTGCTTTGGT 1615420
```

3.1.30 NC_045512.2 SARS-Cov-2 5279-5299:

AACAAGTGTATCTTGCCACT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 5279-5299
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 529      AACAAGTGTATCTTGCCACT 549
          |||| |||| ||||| |||||
Sbjct 2091448 AACACCTGTAATCTTGCCACT 2091468
```

3.1.31 NC_045512.2 SARS-Cov-2 18999-19023:

ATTATTAG-CAGACAAATTCCCAGTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 18999-19023
Score = 31.0 bits (33), Expect = 1.8
Identities = 23/26 (88%), Gaps = 1/26 (4%)
Strand=Plus/Plus
Query 249      ATTATTAG-CAGACAAATTCCCAGTT 273
          ||| |||| |||| ||||| |||||
Sbjct 1052883 ATTTTATAGACAGAAAATTCCCAGTT 1052908
```

3.1.32 NC_045512.2 SARS-Cov-2 29805-29817:

AATGTGTAAAATT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29805-29817
Score = 24.7 bits (26), Expect = 6.3
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus
Query 5      AATGTGAAAATT 17
          |||
Sbjct 21034  AATGTGAAAATT 21046

```

3.1.33 NC_045512.2 SARS-Cov-2 16626-16640:

CAAGCTTTTTGCAGC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 16626-16640
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 876      CAAGCTTTTTGCAGC 890
          |||
Sbjct 2006342  CAAGCTTTTTGCAGC 2006328

```

3.1.34 NC_045512.2 SARS-Cov-2 8561-8583:

GTAAATAATTGGTTGAAGCAGTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8561-8583
Score = 33.7 bits (36), Expect = 0.15
Identities = 21/23 (91%), Gaps = 0/23 (0%)
Strand=Plus/Plus
Query 811      GTAAATAATTGGTTGAAGCAGTT 833
          || || |||
Sbjct 298021  GTGAAAATTGGTTGAAGCAGTT 298043

```

3.1.35 NC_045512.2 SARS-Cov-2 12195-12214:

TTAAAAAGTTGAAGAAGTCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12195-12214
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)

```

```

Strand=Plus/Plus
Query  445      TTAAAAAGTTGAAGAAGTCT  464
          || |||||
Sbjct  146283    TTCAAAGTTGAAGGAGTCT  146302

```

3.1.36 NC_045512.2 SARS-Cov-2 23951-23970:

TTTGGTGGTTTTAATTTTTC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23951-23970
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query  201      TTTGGTGGTTTTAATTTTTC  220
          |||||
Sbjct  429215    TTTGGTGGTTTTCATTCTC  429234

```

3.1.37 NC_045512.2 SARS-Cov-2 12814-12842:

ACTGTT-ATCCGATTTACAGGATTTGAAAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12814-12842
Score = 33.7 bits (36), Expect = 0.15
Identities = 26/30 (87%), Gaps = 1/30 (3%)
Strand=Plus/Minus
Query  64      ACTGTT-ATCCGATTTACAGGATTTGAAAT  92
          ||||| ||||| | |||||
Sbjct  50285    ACTGTTTATCCGATTTGAAAGATTTGAAAT  50256

```

3.1.38 NC_045512.2 SARS-Cov-2 8297-8311:

AACAAAGTTGAAAAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8297-8311
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query  547      AACAAAGTTGAAAAC  561
          |||||
Sbjct  1187901    AACAAAGTTGAAAAC  1187887

```

3.1.39 NC_045512.2 SARS-Cov-2 29463-29481:

CTGCAGATTTGGATGATTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29463-29481
Score = 26.5 bits (28), Expect = 9.5
Identities = 17/19 (89%), Gaps = 0/19 (0%)
Strand=Plus/Minus
Query 13          CTGCAGATTTGGATGATTT 31
          ||| |||
Sbjct 1156350    CTGAAGATTTGGATGAATT 1156332
```

3.1.40 NC_045512.2 SARS-Cov-2 8055-8069:

CGTTTTTCATCAACTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8055-8069
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 305        CGTTTTTCATCAACTT 319
          |||
Sbjct 516444    CGTTTTTCATCAACTT 516430
```

3.1.41 NC_045512.2 SARS-Cov-2 27261-27275:

GACTTTTAAAGTTTC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 27261-27275
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 511        GACTTTTAAAGTTTC 525
          |||
Sbjct 633059    GACTTTTAAAGTTTC 633073
```

3.1.42 NC_045512.2 SARS-Cov-2 15608-15648:

TACAACACAGACTTTATGAGT-GTCTCTATAGAAATAGAGAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15608-15648
Score = 39.2 bits (42), Expect = 0.003
Identities = 36/42 (86%), Gaps = 3/42 (7%)
Strand=Plus/Plus
Query 858      TACAACACAGACTTTATGAGT-GTCTCTATAGAAATAGAGAT 898
          ||||| |||||||||||| ||| |||||||| || |||| ||||
Sbjct 1674709 TACAATACAGACTTTAT-AGTCGTCTCTAAAGGAATA-AGAT 1674748

```

3.1.43 NC_045512.2 SARS-Cov-2 12267-12287:

TGGAAAAGATGGCTGATCAAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12267-12287
Score = 31.0 bits (33), Expect = 1.8
Identities = 20/21 (95%), Gaps = 1/21 (5%)
Strand=Plus/Minus
Query 517      TGGAAAAGATGGCTGATCAAG 537
          |||||||||||||||| ||||
Sbjct 1612918 TGGAAAAGATGGCTGA-CAAG 1612899

```

3.1.44 NC_045512.2 SARS-Cov-2 14330-14349:

ATTGTGTAACTGTTTGGAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 14330-14349
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 580      ATTGTGTAACTGTTTGGAT 599
          ||||| | ||||||||||||
Sbjct 915770 ATTGTTTGAAGTGTGGAT 915751

```

3.1.45 NC_045512.2 SARS-Cov-2 15157-15176:

CAAAAATTATTGAAATCAAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15157-15176
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)

```

```

Strand=Plus/Minus
Query 407      CAAAAATTATTGAAATCAAT 426
          ||||| | |||||
Sbjct 497640   CAAAAGTCATTGAAATCAAT 497621

```

3.1.46 NC_045512.2 SARS-Cov-2 24142-24156:

TTTGCCACCTTTGCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 24142-24156
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 392      TTTGCCACCTTTGCT 406
          |||||
Sbjct 1910772   TTTGCCACCTTTGCT 1910786

```

3.1.47 NC_045512.2 SARS-Cov-2 21947-22005:

AAAGTCTGTGAATTTCAATTTTGTAATGATCCATTTTTGGGTGTTTATTACCACAAAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 21947-22005
Score = 33.7 bits (36), Expect = 0.15
Identities = 44/59 (75%), Gaps = 3/59 (5%)
Strand=Plus/Minus
Query 197      AAAGTCTGTGAATTTCAATTTTGTAATGATCCATTTTTGGGTGTTTATTACCACAAAAA 255
          ||| ||| || |||| |||| | | ||| | | |||| ||||| |||||
Sbjct 1705768   AAATTCTATGCATTTGGATTTTCTGA--ATCGAATGTTGG-TGTTTATTACAATAAAAA 170571

```

3.1.48 NC_045512.2 SARS-Cov-2 727-741:

TGAAGATTTTCAAGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 727-741
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 277      TGAAGATTTTCAAGA 291
          |||||
Sbjct 761380   TGAAGATTTTCAAGA 761366

```

3.1.49 NC_045512.2 SARS-Cov-2 14857-14872:

GTTGAAGTTGTTGATA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 14857-14872
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 107 GTTGAAGTTGTTGATA 122
          |||
Sbjct 52408 GTTGAAGTTGTTGATA 52393
```

3.1.50 NC_045512.2 SARS-Cov-2 693-713:

TTGACTTAGGCGACGAGCTTG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 693-713
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Minus
Query 243 TTGACTTAGGCGACGAGCTTG 263
          |||
Sbjct 1839755 TTGACTTAGGCGATGAACTTG 1839735
```

3.1.51 NC_045512.2 SARS-Cov-2 8237-8251:

TCACATCAATCTGAC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8237-8251
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 487 TCACATCAATCTGAC 501
          |||
Sbjct 457029 TCACATCAATCTGAC 457015
```

3.1.52 NC_045512.2 SARS-Cov-2 8731-8752:

TACAGATACTTGTTTTGCTAAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8731-8752
Score = 36.5 bits (39), Expect = 0.042
Identities = 21/22 (95%), Gaps = 0/22 (0%)
Strand=Plus/Minus
Query 931 TACAGATACTTGTTTTGCTAAC 952
      ||||| |||||
Sbjct 27382 TACAAATACTTGTTTTGCTAAC 27361

```

3.1.53 NC_045512.2 SARS-Cov-2 533-555:

GCAGAACTCGAAGGCATTCAGTA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 533-555
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/23 (87%), Gaps = 0/23 (0%)
Strand=Plus/Minus
Query 83 GCAGAACTCGAAGGCATTCAGTA 105
      ||||| || || |||||
Sbjct 1030975 GCAGAGCTGGAGGGCATTCAGTA 1030953

```

3.1.54 NC_045512.2 SARS-Cov-2 20251-20266:

ATTGATTTCTTAGAAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 20251-20266
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 501 ATTGATTTCTTAGAAT 516
      |||||
Sbjct 1818993 ATTGATTTCTTAGAAT 1818978

```

3.1.55 NC_045512.2 SARS-Cov-2 12054-12073:

TTTGTGAAGAAATGCTGGAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12054-12073
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)

```

```

Strand=Plus/Minus
Query 304      TTTGTGAAGAAATGCTGGAC 323
          ||| ||| |||||
Sbjct 1332501  TTTTGTGAAGAAATGCTGGAC 1332482

```

3.1.56 NC_045512.2 SARS-Cov-2 4921-4935:

CTTTGACAATCTTAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4921-4935
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 171      CTTTGACAATCTTAA 185
          |||||
Sbjct 1889748  CTTTGACAATCTTAA 1889762

```

3.1.57 NC_045512.2 SARS-Cov-2 19354-19368:

TTAAAACAATTACCA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19354-19368
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 604      TTAAAACAATTACCA 618
          |||||
Sbjct 1958680  TTAAAACAATTACCA 1958694

```

3.1.58 NC_045512.2 SARS-Cov-2 28088-28102:

TGGTTCTAAATCACC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 28088-28102
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 338      TGGTTCTAAATCACC 352
          |||||
Sbjct 741034  TGGTTCTAAATCACC 741048

```

3.1.59 NC_045512.2 SARS-Cov-2 29859-29873:

TAGGAGAATGACaaa

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29859-29873
Score = 23.8 bits (25), Expect = 8.9
Identities = 14/15 (93%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 9 TAGGAGAATGACaaa 23
      |||
Sbjct 660033 TAGGAGAATGAGAAA 660019
```

3.1.60 NC_045512.2 SARS-Cov-2 28517-28531:

GACCAAATTGGCTAC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 28517-28531
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 767 GACCAAATTGGCTAC 781
      |||
Sbjct 706227 GACCAAATTGGCTAC 706213
```

3.1.61 NC_045512.2 SARS-Cov-2 1024-1041:

ACCTTTTGAAATTAAATT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1024-1041
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 274 ACCTTTTGAAATTAAATT 291
      || |||
Sbjct 2041303 ACTTTTTGAAATTAAATT 2041320
```

3.1.62 NC_045512.2 SARS-Cov-2 21670-21685:

TTATTACCCTGACAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 21670-21685
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 920      TTATTACCCTGACAAA 935
          |||
Sbjct 1668230 TTATTACCCTGACAAA 1668215

```

3.1.63 NC_045512.2 SARS-Cov-2 14830-14844:

TGTGATATCAGACAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 14830-14844
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 80      TGTGATATCAGACAA 94
          |||
Sbjct 1752307 TGTGATATCAGACAA 1752293

```

3.1.64 NC_045512.2 SARS-Cov-2 1698-1712:

CATCTTTTTCTGCTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1693-1712
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 943      TTTGGCATCTTTTTCTGCTT 962
          ||| |||
Sbjct 241762 TTTGCCATCTTTTTCTCCTT 241743

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1698-1712
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 948      CATCTTTTTCTGCTT 962
          |||

```

Sbjct 327135 CATCTTTTCTGCTT 327121

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350

Query = NC_045512.2 SARS-Cov-2 1693-1712

Score = 28.3 bits (30), Expect = 6.2

Identities = 18/20 (90%), Gaps = 0/20 (0%)

Strand=Plus/Plus

Query 943 TTTGGCATCTTTTCTGCTT 962

|||| |||

Sbjct 1488055 TTGTCATCTTTTCTCCTT 1488074

3.1.65 NC_045512.2 SARS-Cov-2 7337-7358:

TTTATTAGTAATTCTTGGCTTA

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350

Query = NC_045512.2 SARS-Cov-2 7337-7358

Score = 28.3 bits (30), Expect = 6.2

Identities = 20/22 (91%), Gaps = 1/22 (5%)

Strand=Plus/Plus

Query 587 TTTATTAGTAATTCTTGGCTTA 608

||||| ||| |||

Sbjct 609045 TTTAT-AGTTATTCTTGGCTTA 609065

3.1.66 NC_045512.2 SARS-Cov-2 20358-20375:

TGGTTTACATCTACTGAT

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350

Query = NC_045512.2 SARS-Cov-2 20358-20375

Score = 33.7 bits (36), Expect = 0.15

Identities = 18/18 (100%), Gaps = 0/18 (0%)

Strand=Plus/Plus

Query 608 TGGTTTACATCTACTGAT 625

|||||

Sbjct 2138698 TGGTTTACATCTACTGAT 2138715

3.1.67 NC_045512.2 SARS-Cov-2 27900-27914:

TTTCTTGTTTTCTTA

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350

```

Query = NC_045512.2 SARS-Cov-2 27900-27914
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 150      TTTCTTGTTTTCTTA 164
            |||
Sbjct 1598677 TTTCTTGTTTTCTTA 1598663

```

3.1.68 NC_045512.2 SARS-Cov-2 13607-13627:

TCCAAGAAAAGGACGAAGATG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13607-13627
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Minus
Query 857      TCCAAGAAAAGGACGAAGATG 877
            |||
Sbjct 1673267 TCCAAGAAAAGGATGCAGATG 1673247

```

3.1.69 NC_045512.2 SARS-Cov-2 21223-21238:

TGGTGGACAGCCTTTG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 21223-21238
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 473      TGGTGGACAGCCTTTG 488
            |||
Sbjct 1862254 TGGTGGACAGCCTTTG 1862239

```

3.1.70 NC_045512.2 SARS-Cov-2 24943-24963:

TGTTGTAATAGGAATTGTCAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 24943-24963
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Minus
Query 193      TGTTGTAATAGGAATTGTCAA 213

```

```
      |||| | ||||| ||||| |||
Sbjct 619296 TGTCTAATAGGAATTGGCAA 619276
```

3.1.71 NC_045512.2 SARS-Cov-2 20436-20454:

CAGTACAGTTAAAAACTAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 20436-20454
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Minus
Query 686      CAGTACAGTTAAAAACTAT 704
          ||||| | ||||| ||||| |||
Sbjct 753291 CAGTATAGTTAAAAACTAT 753273
```

3.1.72 NC_045512.2 SARS-Cov-2 7511-7533:

AATAGAGCAACAAGAGTCGAATG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7511-7533
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/23 (87%), Gaps = 0/23 (0%)
Strand=Plus/Minus
Query 761      AATAGAGCAACAAGAGTCGAATG 783
          ||| ||| || | ||||| ||||| |||
Sbjct 1640661 AATTGAGGAAGAAGAGTCGAATG 1640639
```

3.1.73 NC_045512.2 SARS-Cov-2 16528-16551:

GTTGGTAGCGATAATGTTACTGAC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 16528-16551
Score = 31.0 bits (33), Expect = 1.8
Identities = 21/24 (88%), Gaps = 0/24 (0%)
Strand=Plus/Minus
Query 778      GTTGGTAGCGATAATGTTACTGAC 801
          ||||| ||||| | ||| |||||
Sbjct 1498616 GTTGGTAGCGAAATTGTTTCTGAC 1498593
```

3.1.74 NC_045512.2 SARS-Cov-2 24619-24639:

AGCTTCTGCTAATCTTGCTGC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 24619-24639
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Minus
Query 869      AGCTTCTGCTAATCTTGCTGC 889
          |||| |
Sbjct 1449163 AGCTACTGCTAATCTTGATGC 1449143

```

3.1.75 NC_045512.2 SARS-Cov-2 20145-20159:

GTTCAATTATTATAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 20145-20159
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 395      GTTCAATTATTATAA 409
          ||
Sbjct 631427 GTTCAATTATTATAA 631441

```

3.1.76 NC_045512.2 SARS-Cov-2 1618-1647:

TGAAATACTCCAAAAAGAGAAAGTCA-ACAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1618-1647
Score = 29.2 bits (31), Expect = 6.2
Identities = 26/31 (84%), Gaps = 4/31 (13%)
Strand=Plus/Minus
Query 868      TGAAATACTCCAAAAAGAGAAAGTCA-ACAT 897
          ||||| |
Sbjct 903088 TGAAATACG---AAAAGAGAAAGTCAGACAT 903061

```

3.1.77 NC_045512.2 SARS-Cov-2 22393-22412:

AAAATATAATGAAAATGGAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22393-22412
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 643      AAAATATAATGAAAATGGAA 662
          || |||||||||||||| ||
Sbjct 2125326 AACATATAATGAAAATGAAA 2125307

```

3.1.78 NC_045512.2 SARS-Cov-2 25443-25458:

AGGTGAAATCAAGGAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 25443-25458
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus
Query 693      AGGTGAAATCAAGGAT 708
          ||||||||||||||
Sbjct 739501 AGGTGAAATCAAGGAT 739516

```

3.1.79 NC_045512.2 SARS-Cov-2 9350-9379:

AATATGTTTACACCACTAATTCAACCTATT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 9350-9379
Score = 28.3 bits (30), Expect = 6.2
Identities = 24/30 (80%), Gaps = 0/30 (0%)
Strand=Plus/Minus
Query 600      AATATGTTTACACCACTAATTCAACCTATT 629
          ||||| ||| || | ||||||||||||
Sbjct 554669 AATATTTTCCATTTCAAATTCAACCTATT 554640

```

3.1.80 NC_045512.2 SARS-Cov-2 18824-18838:

AAGTCCATGGTAATG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 18824-18838
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)

```

```

Strand=Plus/Minus
Query  74      AAGTCCATGGTAATG  88
          |||
Sbjct  228900  AAGTCCATGGTAATG  228886

```

3.1.81 NC_045512.2 SARS-Cov-2 2567-2591:

CAAC-CTACTAGTGAAGCTGTTGAAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2567-2591
Score = 31.0 bits (33), Expect = 1.8
Identities = 23/26 (88%), Gaps = 1/26 (4%)
Strand=Plus/Minus
Query  817      CAAC-CTACTAGTGAAGCTGTTGAAG  841
          ||| ||| ||| |||
Sbjct  1808290  CAACGCTACTCGTGCAGCTGTTGAAG  1808265

```

3.1.82 NC_045512.2 SARS-Cov-2 27336-27353:

TGAGAATAAATATTCTCA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 27336-27353
Score = 33.7 bits (36), Expect = 0.15
Identities = 18/18 (100%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query  586      TGAGAATAAATATTCTCA  603
          |||
Sbjct  2141078  TGAGAATAAATATTCTCA  2141095

```

3.1.83 NC_045512.2 SARS-Cov-2 13938-13959:

AGAAAACCCAGATATATTACGC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13938-13959
Score = 31.9 bits (34), Expect = 0.51
Identities = 20/22 (91%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query  188      AGAAAACCCAGATATATTACGC  209
          || ||| |||
Sbjct  1375694  AGCAAACCGAGATATATTACGC  1375715

```

3.1.84 NC_045512.2 SARS-Cov-2 17680-17694:

CATGATGTTTCATCT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17680-17694
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 930      CATGATGTTTCATCT 944
          |||
Sbjct 781895  CATGATGTTTCATCT 781881
```

3.1.85 NC_045512.2 SARS-Cov-2 28811-28825:

AGTCAAGCCTCTTCT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 28811-28825
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 61      AGTCAAGCCTCTTCT 75
          |||
Sbjct 2011921 AGTCAAGCCTCTTCT 2011935
```

3.1.86 NC_045512.2 SARS-Cov-2 6781-6800:

CTTTACTTTATTGCTACAAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 6781-6800
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 31      CTTTACTTTATTGCTACAAT 50
          ||| |||
Sbjct 267335  CTTTCCTTTATTGCTAAAAT 267316
```

3.1.87 NC_045512.2 SARS-Cov-2 3477-3497:

TTGCAGGAGCCTTAAATAAGG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3477-3497
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 727      TTGCAGGAGCCTTAAATAAGG 747
          || ||||| |||||
Sbjct 633514  TTCCAGGAACCTTAAATAAGG 633534

```

3.1.88 NC_045512.2 SARS-Cov-2 26551-26568:

TTGAAGAGCTTAAAAAGC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 26551-26568
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 801      TTGAAGAGCTTAAAAAGC 818
          |||| |
Sbjct 2098347  TTGATGAGCTTAAAAAGC 2098330

```

3.1.89 NC_045512.2 SARS-Cov-2 29855-29866:

TTCTTAGGAGAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29855-29866
Score = 22.9 bits (24), Expect = 8.9
Identities = 12/12 (100%), Gaps = 0/12 (0%)
Strand=Plus/Minus
Query 5       TTCTTAGGAGAA 16
          |||||
Sbjct 368312  TTCTTAGGAGAA 368301

```

3.1.90 NC_045512.2 SARS-Cov-2 6615-6635:

TAGGTTTGAAAACCCTTGCTA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 6615-6635
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)

```

```

Strand=Plus/Minus
Query 865 TAGGTTTGAAAACCCTTGCTA 885
          |||
Sbjct 1371319 TAGGTTTGAAAAGCTTGCTA 1371299

```

3.1.91 NC_045512.2 SARS-Cov-2 29285-29299:

AAATTGGATGACAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29285-29299
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 535 AAATTGGATGACAAA 549
          |||
Sbjct 936867 AAATTGGATGACAAA 936853

```

3.1.92 NC_045512.2 SARS-Cov-2 27577-27609:

CAATTTGCTTTTGCTTGTCTG-ACGGCGTAAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 27577-27609
Score = 31.9 bits (34), Expect = 0.51
Identities = 28/34 (82%), Gaps = 1/34 (3%)
Strand=Plus/Minus
Query 827 CAATTTGCTTTTGCTTGTCTG-ACGGCGTAAAA 859
          ||| || |||
Sbjct 941 CAATCTGTTTTTGCTTGTCTGATGAAGGGCGTTAAA 908

```

3.1.93 NC_045512.2 SARS-Cov-2 12192-12211:

TTCTTAAAAAGTTGAAGAAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12192-12211
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 442 TTCTTAAAAAGTTGAAGAAG 461
          ||| |||
Sbjct 558372 TTCTAAAAAGTTGAACAAG 558391

```

3.1.94 NC_045512.2 SARS-Cov-2 21546-21564:

TAACAACCTAAACGAACAAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 21546-21564
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Plus
Query 796      TAACAACCTAAACGAACAAT 814
          |||
Sbjct 1318293 TAACAACCTAAACGAAGAAT 1318311
```

3.1.95 NC_045512.2 SARS-Cov-2 26114-26131:

AAGAACATGTCCAAATTC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 26114-26131
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 364      AAGAACATGTCCAAATTC 381
          |||
Sbjct 1806992 AAGAACATGTCAAATTC 1807009
```

3.1.96 NC_045512.2 SARS-Cov-2 26815-26839:

CTTCTTTCAGACTGTTTGCGCGTAC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 26815-26839
Score = 28.3 bits (30), Expect = 6.2
Identities = 21/25 (84%), Gaps = 0/25 (0%)
Strand=Plus/Minus
Query 65      CTTCTTTCAGACTGTTTGCGCGTAC 89
          |||
Sbjct 431298 CTTCTTTCAGAAAGTCTGCGGGTAC 431274
```

3.1.97 NC_045512.2 SARS-Cov-2 15148-15162:

CAGTTTCATCAAAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15148-15162
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 398      CAGTTTCATCAAAAA 412
          |||
Sbjct 559437  CAGTTTCATCAAAAA 559451

```

3.1.98 NC_045512.2 SARS-Cov-2 7822-7848:

TCATTTTGTAACTT-AGACAACCTGAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7822-7848
Score = 30.1 bits (32), Expect = 1.8
Identities = 24/28 (86%), Gaps = 1/28 (4%)
Strand=Plus/Minus
Query 972      TCATTTTGTAACTT-AGACAACCTGAG 998
          ||| | |||| | ||| |||
Sbjct 1165848  TCAGTCTGTTATCTTTAGACAACCTGAG 1165821

```

3.1.99 NC_045512.2 SARS-Cov-2 11762-11782:

AATAGCATAGATGCCTTCAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11762-11782
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Minus
Query 12      AATAGCATAGATGCCTTCAAA 32
          ||| | ||| |||
Sbjct 730476  AATATCATAAATGCCTTCAAA 730456

```

3.1.100 NC_045512.2 SARS-Cov-2 1632-1651:

AAGAGAAAGTCAACATCAAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1632-1651
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)

```

```

Strand=Plus/Minus
Query  882      AAGAGAAAGTCAACATCAAT  901
          ||||| | |||||
Sbjct  975891  AAGAGTACGTCAACATCAAT  975872

```

3.1.101 NC_045512.2 SARS-Cov-2 19759-19774:

ACAACATTACCTGTTA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19759-19774
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query  9      ACAACATTACCTGTTA  24
          |||||
Sbjct  664905  ACAACATTACCTGTTA  664890

```

3.1.102 NC_045512.2 SARS-Cov-2 9781-9800:

TAGTACTTTTGAAGAAGCTG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 9781-9800
Score = 32.8 bits (35), Expect = 0.51
Identities = 19/20 (95%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query  31      TAGTACTTTTGAAGAAGCTG  50
          || |||||
Sbjct  1283169  TATTACTTTTGAAGAAGCTG  1283150

```

3.1.103 NC_045512.2 SARS-Cov-2 16454-16477:

AATCACATAAACCACCCATTAGTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 16454-16477
Score = 31.0 bits (33), Expect = 1.8
Identities = 21/24 (88%), Gaps = 0/24 (0%)
Strand=Plus/Plus
Query  704      AATCACATAAACCACCCATTAGTT  727
          ||||| ||| |||||
Sbjct  1114933  AATCATTTAAAGCACCCATTAGTT  1114956

```

3.1.104 NC_045512.2 SARS-Cov-2 17086-17101:

CCTGGTACTGGTAAGA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17086-17101
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 336 CCTGGTACTGGTAAGA 351
      |||
Sbjct 420220 CCTGGTACTGGTAAGA 420205
```

3.1.105 NC_045512.2 SARS-Cov-2 23896-23910:

CCAAGAAGTTTTTGC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23896-23910
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 146 CCAAGAAGTTTTTGC 160
      |||
Sbjct 581322 CCAAGAAGTTTTTGC 581336
```

3.1.106 NC_045512.2 SARS-Cov-2 3093-3115:

CATCAACTCAATATGAGTATGGT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3093-3115
Score = 33.7 bits (36), Expect = 0.15
Identities = 21/23 (91%), Gaps = 0/23 (0%)
Strand=Plus/Minus
Query 343 CATCAACTCAATATGAGTATGGT 365
      ||| |||
Sbjct 1055874 CATAA ACTCAATATGAGTATAGT 1055852
```

3.1.107 NC_045512.2 SARS-Cov-2 2790-2817:

CTTTTGA ACTTGATGAAAGGATTGATAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2790-2817
Score = 29.2 bits (31), Expect = 6.2
Identities = 23/28 (82%), Gaps = 0/28 (0%)
Strand=Plus/Minus
Query 40 CTTTGAACCTTGATGAAAGGATTGATAA 67
      || ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 53064 CTCTGTACTCGATGTCAGGATTGATAA 53037

```

3.1.108 NC_045512.2 SARS-Cov-2 3918-3938:

GTAAACCTTCAGTTGAACAGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3918-3938
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Minus
Query 168 GTAAACCTTCAGTTGAACAGA 188
      ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 1685667 GTAAACCTTCAGTTGTAAAGA 1685647

```

3.1.109 NC_045512.2 SARS-Cov-2 5862-5881:

TTTTCTACAAAGAAAACAGT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 5862-5881
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 112 TTTTCTACAAAGAAAACAGT 131
      ||| ||| ||| ||| ||| ||| ||| |||
Sbjct 650416 TTTTATACAAAGAAAAGAGT 650397

```

3.1.110 NC_045512.2 SARS-Cov-2 27577-27599:

CAATTTGCTTTTGCTTGTCTGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 27577-27599
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/23 (87%), Gaps = 0/23 (0%)

```

```
Strand=Plus/Minus
Query  977  CAATTTGCTTTTGCTTGCCTGA  999
      |||| || ||||| ||||| |||
Sbjct  941  CAATCTGTTTTTGCTTGCATGA  919
```

3.1.111 NC_045512.2 SARS-Cov-2 21437-21452:

TGTCTTTAAAAGAAGG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  21437-21452
Score = 30.1 bits (32),  Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query  687      TGTCTTTAAAAGAAGG  702
      ||||| ||||| ||||| |||||
Sbjct  2124147  TGTCTTTAAAAGAAGG  2124132
```

3.1.112 NC_045512.2 SARS-Cov-2 3176-3196:

CCTGAAGAAGAGCAAGAAGAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  3176-3196
Score = 34.6 bits (37),  Expect = 0.15
Identities = 20/21 (95%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query  426      CCTGAAGAAGAGCAAGAAGAA  446
      ||||| ||||| ||||| ||||| ||
Sbjct  1148436  CCTGAAGAAGAGCAAGAAAAA  1148456
```

3.1.113 NC_045512.2 SARS-Cov-2 443-457:

GTTTTGCCTCAACTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  443-457
Score = 28.3 bits (30),  Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query  393      GTTTTGCCTCAACTT  407
      ||||| ||||| ||||| |||||
Sbjct  733746  GTTTTGCCTCAACTT  733732
```

3.1.114 NC_045512.2 SARS-Cov-2 17126-17145:

TCTACTACCCTTCTGCTCGC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17126-17145
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 376      TCTACTACCCTTCTGCTCGC 395
          |||
Sbjct 1147296  TCTACTACCCTGCTGCTGGC 1147315
```

3.1.115 NC_045512.2 SARS-Cov-2 7290-7304:

GATTGGCTGCAATCA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7290-7304
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 540      GATTGGCTGCAATCA 554
          |||
Sbjct 87491     GATTGGCTGCAATCA 87477
```

3.1.116 NC_045512.2 SARS-Cov-2 15905-15922:

AGGGTGATGATTATGTGT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15905-15922
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 155      AGGGTGATGATTATGTGT 172
          |||
Sbjct 926675   AGGGTGATGATTATGAGT 926692
```

3.1.117 NC_045512.2 SARS-Cov-2 7791-7811:

GTCAAAAGACTTATGAAAGAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7791-7811
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Minus
Query 41      GTCAAAAGACTTATGAAAGAC 61
          ||| ||| |||||
Sbjct 352120  GTCCAAATACTTATGAAAGAC 352100

```

3.1.118 NC_045512.2 SARS-Cov-2 17436-17451:

CGACCCTGCTCAATTA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17436-17451
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 686      CGACCCTGCTCAATTA 701
          |||||
Sbjct 1323958  CGACCCTGCTCAATTA 1323943

```

3.1.119 NC_045512.2 SARS-Cov-2 9321-9335:

GTGGTGTAGATGCTG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 9321-9335
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 571      GTGGTGTAGATGCTG 585
          |||||
Sbjct 431066  GTGGTGTAGATGCTG 431052

```

3.1.120 NC_045512.2 SARS-Cov-2 3118-3140:

TGAAGATGATTACCAAGGTAAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3118-3140
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/23 (87%), Gaps = 0/23 (0%)

```

```

Strand=Plus/Plus
Query  368      TGAAGATGATTACCAAGGTAAAC  390
      |||||  |||
Sbjct  1070231  TGAAGCGCATTACCAAGGTAAAC  1070253

```

3.1.121 NC_045512.2 SARS-Cov-2 7897-7923:

TGGTAAATCAAAATG-TGAAGAATCATC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7897-7923
Score = 30.1 bits (32), Expect = 1.8
Identities = 24/28 (86%), Gaps = 1/28 (4%)
Strand=Plus/Minus
Query  147      TGGTAAATCAAAATG-TGAAGAATCATC  173
      |||
Sbjct  1909695  TGGTAAATCAAAATGATGTAAATTCATC  1909668

```

3.1.122 NC_045512.2 SARS-Cov-2 23519-23534:

GCTGAACATGTCAACA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23519-23534
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query  769      GCTGAACATGTCAACA  784
      |||
Sbjct  1438634  GCTGAACATGTCAACA  1438619

```

3.1.123 NC_045512.2 SARS-Cov-2 4916-4930:

ATCACCTTTGACAAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4916-4930
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query  166      ATCACCTTTGACAAT  180
      |||
Sbjct  1172942  ATCACCTTTGACAAT  1172956

```

3.1.124 NC_045512.2 SARS-Cov-2 24562-24583:

ACTTCAAAGTTTGCAGACATAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 24562-24583
Score = 31.9 bits (34), Expect = 0.51
Identities = 20/22 (91%), Gaps = 0/22 (0%)
Strand=Plus/Minus
Query 812 ACTTCAAAGTTTGCAGACATAT 833
      |||
Sbjct 688176 ACTTCAAAGTTAGCATACATAT 688155
```

3.1.125 NC_045512.2 SARS-Cov-2 8731-8750:

TACAGATACTTGTTTTGCTA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8731-8750
Score = 32.8 bits (35), Expect = 0.51
Identities = 19/20 (95%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 981 TACAGATACTTGTTTTGCTA 1000
      |||
Sbjct 27382 TACAAATACTTGTTTTGCTA 27363
```

3.1.126 NC_045512.2 SARS-Cov-2 3422-3446:

AAACCAACAGTGGTTGTTAATGCAG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3422-3446
Score = 29.2 bits (31), Expect = 6.2
Identities = 22/25 (88%), Gaps = 1/25 (4%)
Strand=Plus/Minus
Query 672 AAACCAACAGTGGTTGTTAATGCAG 696
      |||
Sbjct 620421 AAACCAACAGTCGTTGTGAA-GCAG 620398
```

3.1.127 NC_045512.2 SARS-Cov-2 19713-19738:

TTACACAAAAGTTGATGGTGTGATG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19713-19738
Score = 35.6 bits (38), Expect = 0.042
Identities = 24/26 (92%), Gaps = 1/26 (4%)
Strand=Plus/Plus
Query 963      TTACACAAAAGTTGATGGTGTGATG 988
                |||
Sbjct 1095304 TTACACAAAAGTTGATGATG-TGATG 1095328

```

3.1.128 NC_045512.2 SARS-Cov-2 2121-2140:

CTGTTTATGAAAACTCAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2121-2140
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 371      CTGTTTATGAAAACTCAA 390
                |||
Sbjct 1775905 CTGTTTATGAAATTCTCAA 1775886

```

3.1.129 NC_045512.2 SARS-Cov-2 2804-2839:

GAAAGGATTGATAAAGTACTTAATGAGAAGTGCTCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2804-2839
Score = 30.1 bits (32), Expect = 1.8
Identities = 28/36 (78%), Gaps = 0/36 (0%)
Strand=Plus/Plus
Query 54      GAAAGGATTGATAAAGTACTTAATGAGAAGTGCTCT 89
                |||
Sbjct 1279965 GAAATGATTGATAAAGTTTTACATGAAAACTGGTCT 1280000

```

3.1.130 NC_045512.2 SARS-Cov-2 19906-19924:

ATATCTACTATTGGTGTTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19906-19924
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)

```

```

Strand=Plus/Minus
Query 156      ATATCTACTATTGGTGTTT 174
          ||||| |||||
Sbjct 1534259 ATATCTGCTATTGGTGTTT 1534241

```

3.1.131 NC_045512.2 SARS-Cov-2 22934-22962:

AAGTCTAATCTCAAACCTTTTGAGAGAGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22934-22962
Score = 31.0 bits (33), Expect = 1.8
Identities = 24/29 (83%), Gaps = 0/29 (0%)
Strand=Plus/Minus
Query 184      AAGTCTAATCTCAAACCTTTTGAGAGAGA 212
          || ||||| | || | |||||
Sbjct 1419452 AATTCTAATCGCCAAACCTTTTGAGAGAGA 1419424

```

3.1.132 NC_045512.2 SARS-Cov-2 22158-22180:

GTTATTTTAAAATATATTCTAAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22145-22180
Score = 32.8 bits (35), Expect = 0.51
Identities = 30/37 (81%), Gaps = 1/37 (3%)
Strand=Plus/Minus
Query 395      AAGAATATTGATG-GTTATTTTAAAATATATTCTAAG 430
          ||||| |||  || ||||| || |||
Sbjct 1807011 AAGAATTTTGACATGTTCTTTTAAAATATAGTCCAAG 1806975

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22158-22180
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/23 (87%), Gaps = 0/23 (0%)
Strand=Plus/Minus
Query 8        GTTATTTTAAAATATATTCTAAG 30
          || | ||||| || |||
Sbjct 1806997 GTTCTTTTAAAATATAGTCCAAG 1806975

```

3.1.133 NC_045512.2 SARS-Cov-2 2913-2930:

TGCAACCAGTATCTGAAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2913-2930
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 163      TGCAACCAGTATCTGAAT 180
          ||||| |||||
Sbjct 2123336 TGCAAGCAGTATCTGAAT 2123319
```

3.1.134 NC_045512.2 SARS-Cov-2 18627-18642:

GTATTTTGTGAAAATA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 18627-18642
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 877      GTATTTTGTGAAAATA 892
          |||||
Sbjct 78641     GTATTTTGTGAAAATA 78626
```

3.1.135 NC_045512.2 SARS-Cov-2 11981-11995:

GAAGCCTTTGAAAAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11981-11995
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 231      GAAGCCTTTGAAAAA 245
          |||||
Sbjct 1210323 GAAGCCTTTGAAAAA 1210309
```

3.1.136 NC_045512.2 SARS-Cov-2 11418-11433:

TTTATAAAGTTTATTA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11418-11433
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 668      TTTATAAAGTTTATTA 683
          |||
Sbjct 1217541  TTTATAAAGTTTATTA 1217526

```

3.1.137 NC_045512.2 SARS-Cov-2 12494-12513:

TATAACACATATAAAAATAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12494-12513
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 744      TATAACACATATAAAAATAC 763
          ||| ||| |||
Sbjct 525344  TATCACACTTATAAAAATAC 525363

```

3.1.138 NC_045512.2 SARS-Cov-2 13888-13902:

AATTGTTGTGATGAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13888-13902
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 138      AATTGTTGTGATGAT 152
          |||
Sbjct 1585876  AATTGTTGTGATGAT 1585890

```

3.1.139 NC_045512.2 SARS-Cov-2 13924-13947:

TGGTATGATTTTGTAGAAAACCCA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13924-13947
Score = 35.6 bits (38), Expect = 0.042
Identities = 22/24 (92%), Gaps = 0/24 (0%)

```

```

Strand=Plus/Plus
Query 174      TGGTATGATTTTGTAGAAAACCCA 197
                |||
Sbjct 1636461 TGGTATGATTTTGTAGAAAATCCA 1636484

```

3.1.140 NC_045512.2 SARS-Cov-2 7063-7077:

CAGAGAAGGCTATTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7063-7077
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 313      CAGAGAAGGCTATTT 327
                |||
Sbjct 1943727 CAGAGAAGGCTATTT 1943713

```

3.1.141 NC_045512.2 SARS-Cov-2 12933-12954:

CTAAAGTGAAGTATTTATACTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12933-12954
Score = 28.3 bits (30), Expect = 6.2
Identities = 20/22 (91%), Gaps = 1/22 (5%)
Strand=Plus/Minus
Query 183      CTAAAGTGAAGTATTTATACTT 204
                |||
Sbjct 59411    CTAAA-TGAAGTATTTATAATT 59391

```

3.1.142 NC_045512.2 SARS-Cov-2 12060-12074:

AAGAAATGCTGGACA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12060-12074
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 310      AAGAAATGCTGGACA 324
                |||
Sbjct 604892    AAGAAATGCTGGACA 604906

```

3.1.143 NC_045512.2 SARS-Cov-2 12269-12289:

GAAAAGATGGCTGATCAAGCT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12269-12289
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 519      GAAAAGATGGCTGATCAAGCT 539
          |||
Sbjct 152922   GAAAAGATGGCTGATGAATCT 152942
```

3.1.144 NC_045512.2 SARS-Cov-2 3942-3965:

AACAAGATGATAAGAAAATCAAAG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3942-3965
Score = 31.0 bits (33), Expect = 1.8
Identities = 21/24 (88%), Gaps = 0/24 (0%)
Strand=Plus/Minus
Query 192      AACAAGATGATAAGAAAATCAAAG 215
          || |||
Sbjct 1647590   AAGAAGAAGAAAAGAAAATCAAAG 1647567
```

3.1.145 NC_045512.2 SARS-Cov-2 11988-12019:

TTGAAAAAATGGTTTCACTACTTTCTGTTTTG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11988-12019
Score = 31.9 bits (34), Expect = 0.51
Identities = 26/32 (81%), Gaps = 0/32 (0%)
Strand=Plus/Plus
Query 238      TTGAAAAAATGGTTTCACTACTTTCTGTTTTG 269
          |||
Sbjct 1287268   TTGAAAAGTTCTTTTAATATTTTCTGTTTTG 1287299
```

3.1.146 NC_045512.2 SARS-Cov-2 18128-18148:

ACACTAAATTCAAAACTGAAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 18128-18148
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Minus
Query 378      ACACTAAATTCAAAACTGAAG 398
            |||
Sbjct 1414826 ACACTAAATTCAAAGGTGAAG 1414806

```

3.1.147 NC_045512.2 SARS-Cov-2 14769-14787:

TCAGGATGGTAATGCTGCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 14769-14787
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Plus
Query 19      TCAGGATGGTAATGCTGCT 37
            |||
Sbjct 2133560 TCAGGATGGTAAAGCTGCT 2133578

```

3.1.148 NC_045512.2 SARS-Cov-2 12004-12023:

ACTACTTTCTGTTTTGCTTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12004-12023
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 254     ACTACTTTCTGTTTTGCTTT 273
            |||
Sbjct 1298293 ACTACTTTCTGAATTGCTTT 1298312

```

3.1.149 NC_045512.2 SARS-Cov-2 28-47:

CAAACCAACCAACTTTTCGAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 28-47
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)

```

```

Strand=Plus/Plus
Query 28      CAAACCAACCAACTTTCGAT 47
          |||
Sbjct 2093116 CAAACCAACCAAGTATCGAT 2093135

```

3.1.150 NC_045512.2 SARS-Cov-2 4204-4230:

AGCGAAAGCTTTGAGAAAAGT-GCCAAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4204-4230
Score = 28.3 bits (30), Expect = 6.2
Identities = 24/29 (83%), Gaps = 2/29 (7%)
Strand=Plus/Plus
Query 454      AGCGAAAGCTTTGAGAAAAGT--GCCAAC 480
          ||| || |||
Sbjct 1014510  AGCAAAGGCTTTGAGAAAAGTACTGCCAAC 1014538

```

3.1.151 NC_045512.2 SARS-Cov-2 4749-4763:

AAACACCTGAAGAAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4749-4763
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 949      AAACACCTGAAGAAC 963
          |||
Sbjct 1727250  AAACACCTGAAGAAC 1727236

```

3.1.152 NC_045512.2 SARS-Cov-2 7569-7583:

ATGTCTATGCTAATG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7569-7583
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 819      ATGTCTATGCTAATG 833
          |||
Sbjct 1321020  ATGTCTATGCTAATG 1321006

```

3.1.153 NC_045512.2 SARS-Cov-2 12993-13012:

TTGGTAGTTTAGCTGCCACA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12993-13012
Score = 32.8 bits (35), Expect = 0.51
Identities = 19/20 (95%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 243      TTGGTAGTTTAGCTGCCACA 262
          ||||| |||||
Sbjct 1918768 TTGGTAATTTAGCTGCCACA 1918787
```

3.1.154 NC_045512.2 SARS-Cov-2 14981-15013:

TTTATTATGATTCAATGAGTTATGAGGATCAAG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 14981-15013
Score = 35.6 bits (38), Expect = 0.042
Identities = 28/33 (85%), Gaps = 2/33 (6%)
Strand=Plus/Plus
Query 231      TTTATTATGATTCAATGAGTTATGAGGATCAAG 263
          ||||| ||| | |||||
Sbjct 1279767 TTTATTATGAA--ATTGAGTTATGAGGATAAAG 1279797
```

3.1.155 NC_045512.2 SARS-Cov-2 22823-22837:

TATAATTATAAATTA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22823-22837
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 73      TATAATTATAAATTA 87
          |||||
Sbjct 1707040 TATAATTATAAATTA 1707026
```

3.1.156 NC_045512.2 SARS-Cov-2 3875-3895:

GCTGAGATTCCTAAAGAGGAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3875-3895
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 125      GCTGAGATTCCTAAAGAGGAA 145
          |||||  |||||
Sbjct 642631  GCTGAGAAACCTAAAGAGGAA 642651

```

3.1.157 NC_045512.2 SARS-Cov-2 20151-20168:

TTATTATAAGAAAGTTGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 20151-20168
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 401      TTATTATAAGAAAGTTGA 418
          |||  |||||
Sbjct 1342071  TTATAATAAGAAAGTTGA 1342054

```

3.1.158 NC_045512.2 SARS-Cov-2 28953-28978:

TGAACCAGCTTGAGAGCAAAATGTCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 28948-28978
Score = 31.0 bits (33), Expect = 1.8
Identities = 26/31 (84%), Gaps = 1/31 (3%)
Strand=Plus/Plus
Query 198      CAGATTGAACCAGCTTGAGAGCAAAATGTCT 228
          ||||  |||||  |||  |  |||||
Sbjct 1424304  CAGAT-GAACCAGCTTGAGCTCCTAATGTCT 1424333

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 28953-28978
Score = 30.1 bits (32), Expect = 1.7
Identities = 22/26 (85%), Gaps = 0/26 (0%)
Strand=Plus/Plus
Query 3        TGAACCAGCTTGAGAGCAAAATGTCT 28
          |||||  |||||  |  |||||

```

Sbjct 1424308 TGAACCAGCTTGAGCTCCTAATGTCT 1424333

3.1.159 NC_045512.2 SARS-Cov-2 19986-20009:

TTTTGATGGTAGAGTTGATGGTCA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19986-20009
Score = 31.9 bits (34), Expect = 0.51
Identities = 22/24 (92%), Gaps = 1/24 (4%)
Strand=Plus/Plus
Query 236      TTTTGATGGTAGAGTTGATGGTCA 259
          |||
Sbjct 631262  TTTTGATGGTAGAGGT-ATGGTCA 631284
```

3.1.160 NC_045512.2 SARS-Cov-2 29816-29839:

TTAATTTTAGTAGTGCTATCCCCA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29816-29839
Score = 26.5 bits (28), Expect = 2.9
Identities = 20/24 (83%), Gaps = 0/24 (0%)
Strand=Plus/Minus
Query 66      TTAATTTTAGTAGTGCTATCCCCA 89
          |||
Sbjct 741405  TTAATTTTAGTCGTATTAACCCCA 741382
```

3.1.161 NC_045512.2 SARS-Cov-2 7652-7670:

ACATTTATTAGTGATGAAG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7652-7670
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Plus
Query 902      ACATTTATTAGTGATGAAG 920
          |||
Sbjct 724225  ACATTTGTTAGTGATGAAG 724243
```

3.1.162 NC_045512.2 SARS-Cov-2 8217-8239:

TTGTTGAATGTCTTAAATTGTCA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8217-8239
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/23 (87%), Gaps = 0/23 (0%)
Strand=Plus/Plus
Query 467      TTGTTGAATGTCTTAAATTGTCA 489
          |||||  || | |||||
Sbjct 1771372  TTGTTGTATTTATTAAATTGTCA 1771394
```

3.1.163 NC_045512.2 SARS-Cov-2 8187-8201:

TTGTTGATTCAGATG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8187-8201
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 437      TTGTTGATTCAGATG 451
          |||||
Sbjct 1673324  TTGTTGATTCAGATG 1673310
```

3.1.164 NC_045512.2 SARS-Cov-2 9829-9848:

AATGTATCTAAAGTTGCGTA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 9829-9848
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 79      AATGTATCTAAAGTTGCGTA 98
          ||| |||||
Sbjct 1719655  AATTTATCTAAAGTTGCATA 1719674
```

3.1.165 NC_045512.2 SARS-Cov-2 4218-4232:

GAAAAGTGCCAACAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4218-4232
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 468      GAAAAGTGCCAACAG 482
          |||
Sbjct 1258685  GAAAAGTGCCAACAG 1258671

```

3.1.166 NC_045512.2 SARS-Cov-2 15898-15915:

GTAAACAGGGTGATGAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15898-15915
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 148      GTAAACAGGGTGATGAT 165
          |||
Sbjct 1936476  GTAAATAGGGTGATGAT 1936493

```

3.1.167 NC_045512.2 SARS-Cov-2 1530-1549:

ATTGGGTTCCACGTGCTAGC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1530-1549
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 780      ATTGGGTTCCACGTGCTAGC 799
          |||
Sbjct 1947129  ATTGGGTTCCAAGTGTTAGC 1947148

```

3.1.168 NC_045512.2 SARS-Cov-2 21725-21744:

TTCTTACCTTTCTTTTCCAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 21725-21744
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)

```

```

Strand=Plus/Minus
Query  975      TTCTTACCTTTCTTTTCCAA  994
          |||||  |||||
Sbjct  551486    TTCTTTACTTTCTTTTCCAA  551467

```

3.1.169 NC_045512.2 SARS-Cov-2 14451-14465:

TGTTCCATTTGTAGT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query  = NC_045512.2 SARS-Cov-2  14451-14465
Score  = 28.3 bits (30),  Expect  = 6.2
Identities  = 15/15 (100%), Gaps  = 0/15 (0%)
Strand=Plus/Minus
Query  701      TGTTCCATTTGTAGT  715
          |||||
Sbjct  1056454  TGTTCCATTTGTAGT  1056440

```

3.1.170 NC_045512.2 SARS-Cov-2 28885-28903:

AACTTCTCCTGCTAGAATG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query  = NC_045512.2 SARS-Cov-2  28885-28903
Score  = 31.0 bits (33),  Expect  = 1.8
Identities  = 18/19 (95%), Gaps  = 0/19 (0%)
Strand=Plus/Plus
Query  135      AACTTCTCCTGCTAGAATG  153
          || |||||
Sbjct  1535620  AATTCTCCTGCTAGAATG  1535638

```

3.1.171 NC_045512.2 SARS-Cov-2 23166-23189:

AAAACAAATGTGTCAATTTCAACT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query  = NC_045512.2 SARS-Cov-2  23166-23189
Score  = 31.0 bits (33),  Expect  = 1.8
Identities  = 21/24 (88%), Gaps  = 0/24 (0%)
Strand=Plus/Plus
Query  416      AAAACAAATGTGTCAATTTCAACT  439
          ||||| |||||
Sbjct  156074  AAAACAAATGAAACAATTTCAACT  156097

```

3.1.172 NC_045512.2 SARS-Cov-2 20566-20585:

AAGGTTGTCAAAGTGACTAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 20566-20585
Score = 29.2 bits (31), Expect = 6.2
Identities = 19/20 (95%), Gaps = 1/20 (5%)
Strand=Plus/Plus
Query 816      AAGGTTGTCAAAGTGACTAT 835
          ||||| |||||
Sbjct 553699  AAGGT-GTCAAAGTGACTAT 553717

```

3.1.173 NC_045512.2 SARS-Cov-2 10603-10617:

ACCTTTTGTGACAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 10600-10617
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 850      TGGACCTTTTGTGACAG 867
          || |||||
Sbjct 1818892  TGCACCTTTTGTGACAG 1818909

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 10603-10617
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 3        ACCTTTTGTGACAG 17
          |||||
Sbjct 1818895  ACCTTTTGTGACAG 1818909

```

3.1.174 NC_045512.2 SARS-Cov-2 18628-18645:

TATTTTGTGAAAATAGGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 18628-18645
Score = 29.2 bits (31), Expect = 6.2

```

Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus
 Query 878 TATTTTGTGAAAATAGGA 895
 ||||| |||||
 Sbjct 2121871 TATTTTTTGTGAAAATAGGA 2121888

3.1.175 NC_045512.2 SARS-Cov-2 17042-17064:

ATCAAAAGG-TTGGTATGCAAAAG

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 17042-17064
 Score = 30.1 bits (32), Expect = 1.8
 Identities = 22/25 (88%), Gaps = 2/25 (8%)
 Strand=Plus/Plus
 Query 292 ATCAAAAGG--TTGGTATGCAAAAG 314
 ||||| || |||||
 Sbjct 1868347 ATCAAAGGGTTTGGTATGCAAAAG 1868371

3.1.176 NC_045512.2 SARS-Cov-2 15117-15131:

TGTCTCTATCTGTAG

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 15117-15131
 Score = 28.3 bits (30), Expect = 6.2
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus
 Query 367 TGTCTCTATCTGTAG 381
 |||||
 Sbjct 1375971 TGTCTCTATCTGTAG 1375985

3.1.177 NC_045512.2 SARS-Cov-2 5998-6017:

AATTGATCTTGTACCAAACC

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 5998-6017
 Score = 32.8 bits (35), Expect = 0.51
 Identities = 19/20 (95%), Gaps = 0/20 (0%)
 Strand=Plus/Minus
 Query 248 AATTGATCTTGTACCAAACC 267
 |||||
 Sbjct 1082334 AATTGATCTTGTACCAATCC 1082315

3.1.178 NC_045512.2 SARS-Cov-2 13701-13720:

TAATTTACTTAAGGATTGTC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13701-13720
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query  951    TAATTTACTTAAGGATTGTC  970
          |||||  |||||
Sbjct  39213   TAATTTGGTTAAGGATTGTC  39194
```

3.1.179 NC_045512.2 SARS-Cov-2 23986-24004:

TCCATCAAAACCAAGCAAG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23986-24004
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Minus
Query  236    TCCATCAAAACCAAGCAAG  254
          |||||
Sbjct  302499  TCCATCAAAACCAAGGAAG  302481
```

3.1.180 NC_045512.2 SARS-Cov-2 3945-3964:

AAGATGATAAGAAAATCAAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3945-3964
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query  195    AAGATGATAAGAAAATCAAA  214
          || |||  |||||
Sbjct  1091829 AACATGAAAAGAAAATCAAA  1091848
```

3.1.181 NC_045512.2 SARS-Cov-2 2297-2315:

TTCTTTAAGCTTGTAATA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2297-2315
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Plus
Query 547      TTCTTTAAGCTTGTAATA 565
          |||||  |||
Sbjct 870607  TTCTTTTAGCTTGTAATA 870625

```

3.1.182 NC_045512.2 SARS-Cov-2 12615-12634:

ACAATTCACCTAATTTAGCA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12615-12634
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 865      ACAATTCACCTAATTTAGCA 884
          |||
Sbjct 1290916  ACAATTCACCTAATGCAGCA 1290935

```

3.1.183 NC_045512.2 SARS-Cov-2 10651-10665:

TATTACAGTTAATGT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 10651-10665
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 901      TATTACAGTTAATGT 915
          |||
Sbjct 1734590  TATTACAGTTAATGT 1734576

```

3.1.184 NC_045512.2 SARS-Cov-2 17828-17849:

AAACTGTTGATTCATCACAGGG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17828-17849
Score = 31.9 bits (34), Expect = 0.51
Identities = 20/22 (91%), Gaps = 0/22 (0%)

```

```

Strand=Plus/Minus
Query  78      AAACTGTTGATTCATCACAGG  99
          |||
Sbjct  1566964  AAACTGTTGATTCAGCACCGG  1566943

```

3.1.185 NC_045512.2 SARS-Cov-2 8750-8764:

AACAAACATGCTGAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8750-8764
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query  950      AACAAACATGCTGAT  964
          |||
Sbjct  716937  AACAAACATGCTGAT  716951

```

3.1.186 NC_045512.2 SARS-Cov-2 11035-11054:

ACTTTTAGTTTTAGTCCAGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11035-11054
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query  285      ACTTTTAGTTTTAGTCCAGA  304
          |||
Sbjct  1553777  ACTTTTAGTTTTGACCAGA  1553758

```

3.1.187 NC_045512.2 SARS-Cov-2 1623-1643:

TACTCCAAAAAGAGAAAGTCA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1623-1643
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Minus
Query  873      TACTCCAAAAAGAGAAAGTCA  893
          |||
Sbjct  158992  TACTCCAAAAAGATAAAGACA  158972

```

3.1.188 NC_045512.2 SARS-Cov-2 1277-1296:

AAAGCCACTTGCGAATTTTG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1277-1296
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 527      AAAGCCACTTGCGAATTTTG 546
          |||
Sbjct 843585   AAAGCCACTTGCGAGTTGTG 843566
```

3.1.189 NC_045512.2 SARS-Cov-2 12398-12417:

CTCAACAACATTATCAACAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12398-12417
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 648      CTCAACAACATTATCAACAA 667
          |||
Sbjct 1623823  CTCAATACCATTATCAACAA 1623842
```

3.1.190 NC_045512.2 SARS-Cov-2 2808-2827:

GGATTGATAAAGTACTTAAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2807-2827
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Minus
Query 57      AGGATTGATAAAGTACTTAAT 77
          |||
Sbjct 1300354  AGGGTGGATAAAGTACTTAAT 1300334
```

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2808-2827
Score = 28.3 bits (30), Expect = 6.2
```

Identities = 18/20 (90%), Gaps = 0/20 (0%)
 Strand=Plus/Minus
 Query 58 GGATTGATAAAGTACTTAAT 77
 ||| |||
 Sbjct 2091374 GGAGTGATAAAGTACGTAAT 2091355

3.1.191 NC_045512.2 SARS-Cov-2 16055-16072:

ATCCTAATCAGGAGTATG

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 16055-16072
 Score = 29.2 bits (31), Expect = 6.2
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Plus
 Query 305 ATCCTAATCAGGAGTATG 322
 |||| |||
 Sbjct 1207707 ATCCAAATCAGGAGTATG 1207724

3.1.192 NC_045512.2 SARS-Cov-2 29844-29864:

ATTTTAATAGCTTCTTAGGAG

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 29844-29864
 Score = 25.6 bits (27), Expect = 6.3
 Identities = 18/21 (86%), Gaps = 0/21 (0%)
 Strand=Plus/Minus
 Query 44 ATTTTAATAGCTTCTTAGGAG 64
 ||||| || |||
 Sbjct 710551 ATTTTCATCTCTTCTTAGGAG 710531

3.1.193 NC_045512.2 SARS-Cov-2 2574-2588:

CTAGTGAAGCTGTTG

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 2574-2588
 Score = 28.3 bits (30), Expect = 6.2
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus
 Query 824 CTAGTGAAGCTGTTG 838
 |||||
 Sbjct 605891 CTAGTGAAGCTGTTG 605905

3.1.194 NC_045512.2 SARS-Cov-2 29378-29397:

AAAAAGGACAAAAAGAAGAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29378-29397
Score = 32.8 bits (35), Expect = 0.51
Identities = 19/20 (95%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 628      AAAAAAGGACAAAAAGAAGAA 647
          || |||
Sbjct 835709   AAGAAGGACAAAAAGAAGAA 835728

```

3.1.195 NC_045512.2 SARS-Cov-2 5824-5838:

TACAAAGTCCTCAGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 5824-5838
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 74      TACAAAGTCCTCAGA 88
          |||
Sbjct 453890   TACAAAGTCCTCAGA 453876

```

3.1.196 NC_045512.2 SARS-Cov-2 3181-3213:

AGAAGAGCAAGAAGAA-GATTGGTTAGATGATGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3181-3213
Score = 28.3 bits (30), Expect = 6.2
Identities = 28/34 (82%), Gaps = 2/34 (6%)
Strand=Plus/Minus
Query 431      AGAAGAGCAAGAAGAA-GATTGGTTAGATGATGA 463
          ||| ||| ||| || |||
Sbjct 1922317   AGAAGAT-AAGATGAAAGAGAGGTTAGATGATGA 1922285

```

3.1.197 NC_045512.2 SARS-Cov-2 18453-18467:

TAAACCACCGCCTGG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 18453-18467
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 703      TAAACCACCGCCTGG 717
          |||
Sbjct 278774  TAAACCACCGCCTGG 278760

```

3.1.198 NC_045512.2 SARS-Cov-2 12881-12895:

TATACAGAACTGGAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12881-12895
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 131      TATACAGAACTGGAA 145
          |||
Sbjct 1293919  TATACAGAACTGGAA 1293933

```

3.1.199 NC_045512.2 SARS-Cov-2 1258-1277:

GCAGACGGGCGATTTTGTTA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1258-1277
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 508      GCAGACGGGCGATTTTGTTA 527
          || || |||
Sbjct 1253416  GCTGATGGGCGATTTTGTTA 1253397

```

3.1.200 NC_045512.2 SARS-Cov-2 1123-1137:

AAGGGTTGAAAAGAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1123-1137
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)

```

```

Strand=Plus/Minus
Query  373      AAGGGTTGAAAAGAA  387
          |||
Sbjct  1333945  AAGGGTTGAAAAGAA  1333931

```

3.1.201 NC_045512.2 SARS-Cov-2 24278-24292:

TTTAATGGTATTGGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  24278-24292
Score = 28.3 bits (30),  Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query  528      TTTAATGGTATTGGA  542
          |||
Sbjct  899190  TTTAATGGTATTGGA  899204

```

3.1.202 NC_045512.2 SARS-Cov-2 6515-6532:

TTAAAAATTACAGAAGAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  6515-6532
Score = 29.2 bits (31),  Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query  765      TTAAAAATTACAGAAGAG  782
          ||| |||
Sbjct  1678193  TTAAAGATTACAGAAGAG  1678176

```

3.1.203 NC_045512.2 SARS-Cov-2 16500-16518:

AGTTTTTTGGTTTATATAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  16500-16518
Score = 31.0 bits (33),  Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Plus
Query  750      AGTTTTTTGGTTTATATAAA  768
          ||| |||
Sbjct  702872  AGTTTTTTGGTTTATATAAA  702890

```

3.1.204 NC_045512.2 SARS-Cov-2 11141-11156:

ATGATGTTTGTCAAAC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11141-11156
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 391      ATGATGTTTGTCAAAC 406
          |||
Sbjct 851116   ATGATGTTTGTCAAAC 851101
```

3.1.205 NC_045512.2 SARS-Cov-2 25921-25953:

AGTCCTATTTCTG—AACATGACTACCAGATTGGT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 25921-25953
Score = 32.8 bits (35), Expect = 0.51
Identities = 29/36 (81%), Gaps = 3/36 (8%)
Strand=Plus/Minus
Query 171      AGTCCTATTTCTG---AACATGACTACCAGATTGGT 203
          |||
Sbjct 1477441   AGTCCTTTTTCAGCCAAAATGATTACCAGATTGGT 1477406
```

3.1.206 NC_045512.2 SARS-Cov-2 3677-3692:

TTTAATCAGCACGAAG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3677-3692
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus
Query 927      TTTAATCAGCACGAAG 942
          |||
Sbjct 953903   TTTAATCAGCACGAAG 953918
```

3.1.207 NC_045512.2 SARS-Cov-2 11478-11495:

TCTCTGTTACTTCTAACT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11478-11495
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 728      TCTCTGTTACTTCTAACT 745
          |||| |
Sbjct 513585  TCTCAGTTACTTCTAACT 513568

```

3.1.208 NC_045512.2 SARS-Cov-2 25007-25032:

AAGGAGGAG-TTAGATAAATATTTTAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 25007-25032
Score = 32.8 bits (35), Expect = 0.51
Identities = 24/27 (89%), Gaps = 1/27 (4%)
Strand=Plus/Plus
Query 257      AAGGAGGAG-TTAGATAAATATTTTAA 282
          |||| |
Sbjct 8515     AAGGATGAGATTAGATAAATATTTAAA 8541

```

3.1.209 NC_045512.2 SARS-Cov-2 23069-23083:

GTTGGTTACCAACCA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23069-23083
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 319      GTTGGTTACCAACCA 333
          |||| |
Sbjct 1430818  GTTGGTTACCAACCA 1430804

```

3.1.210 NC_045512.2 SARS-Cov-2 14859-14874:

TGAAGTTGTTGATAAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 14859-14874
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)

```

```

Strand=Plus/Minus
Query 109      TGAAGTTGTTGATAAG 124
              |||
Sbjct 1303887 TGAAGTTGTTGATAAG 1303872

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350

```

```

Query = NC_045512.2 SARS-Cov-2 14843-14874
Score = 29.2 bits (31), Expect = 6.2
Identities = 26/32 (81%), Gaps = 2/32 (6%)
Strand=Plus/Minus

```

```

Query 93      AACTACTATTTGTAGTTGAAGTTGTTGATAAG 124
              ||| || ||| ||| ||| |||
Sbjct 1570829 AACACAATTTGC--TTGAAATTGTTGATAAG 1570800

```

3.1.211 NC_045512.2 SARS-Cov-2 27336-27350:

TGAGAATAAATATTC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350

```

```

Query = NC_045512.2 SARS-Cov-2 27336-27350
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus

```

```

Query 986      TGAGAATAAATATTC 1000
              |||
Sbjct 2141078 TGAGAATAAATATTC 2141092

```

3.1.212 NC_045512.2 SARS-Cov-2 27753-27778:

AGAATGATTGAACTTTCATTAATTGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350

```

```

Query = NC_045512.2 SARS-Cov-2 27753-27778
Score = 30.1 bits (32), Expect = 1.8
Identities = 22/26 (85%), Gaps = 0/26 (0%)
Strand=Plus/Minus

```

```

Query 3      AGAATGATTGAACTTTCATTAATTGA 28
              ||| ||| ||| ||| ||| |||
Sbjct 1066094 AGAATGATTGAACTATAGTAAATTGA 1066069

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350

```

```

Query = NC_045512.2 SARS-Cov-2 27750-27778
Score = 31.0 bits (33), Expect = 1.8
Identities = 24/29 (83%), Gaps = 0/29 (0%)
Strand=Plus/Minus
Query 950      GACAGAATGATTGAACTTTCATTAATTGA 978
              || |||||
Sbjct 1066097  GATAGAATGATTGAACTATAGTAAATTGA 1066069

```

3.1.213 NC_045512.2 SARS-Cov-2 12230-12246:

TCTGAATTTGACCGTGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12230-12246
Score = 31.9 bits (34), Expect = 0.51
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus
Query 480      TCTGAATTTGACCGTGA 496
              |||||
Sbjct 1808418  TCTGAATTTGACCGTGA 1808402

```

3.1.214 NC_045512.2 SARS-Cov-2 29532-29548:

AAACTCATGCAGACCAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29532-29548
Score = 27.4 bits (29), Expect = 9.5
Identities = 16/17 (94%), Gaps = 0/17 (0%)
Strand=Plus/Minus
Query 82      AAACTCATGCAGACCAC 98
              |||||
Sbjct 701664  AAACTCATGCAGACCAC 701648

```

3.1.215 NC_045512.2 SARS-Cov-2 11838-11861:

TACAGTCTAAAATGTCAGATGTAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11838-11861
Score = 31.9 bits (34), Expect = 0.51
Identities = 22/24 (92%), Gaps = 1/24 (4%)
Strand=Plus/Minus
Query 88      TACAGTCTAAAATGTCAGATGTAA 111

```

```
|||||
Sbjct 897475 TACAGTCTAAAATGTC-GATATAA 897453
```

3.1.216 NC_045512.2 SARS-Cov-2 24627-24647:

CTAATCTTGCTGCTACTAAAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 24627-24647
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 877 CTAATCTTGCTGCTACTAAAA 897
      ||||| | |||||
Sbjct 116880 CTAATCTAGTTGCTACTAAAA 116900
```

3.1.217 NC_045512.2 SARS-Cov-2 1788-1817:

ATTTTAAAGTTACAAAAGGAAAAGCTAAAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1788-1817
Score = 28.3 bits (30), Expect = 6.2
Identities = 24/30 (80%), Gaps = 0/30 (0%)
Strand=Plus/Plus
Query 38 ATTTTAAAGTTACAAAAGGAAAAGCTAAAA 67
      ||| || ||||| ||| |||
Sbjct 267781 ATTCTATAGTTACAAAAGAAAATTTTAAAA 267810
```

3.1.218 NC_045512.2 SARS-Cov-2 15912-15937:

TGATTATGTGTA-CCTTCCTTACCCAG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15912-15937
Score = 29.2 bits (31), Expect = 6.2
Identities = 24/27 (89%), Gaps = 2/27 (7%)
Strand=Plus/Minus
Query 162 TGATTATGTGTA-CCTTCCTTACCCAG 187
      |||| | || |||||
Sbjct 1705313 TGATTTTG-GTATCCTTCCTTACCCAG 1705288
```

3.1.219 NC_045512.2 SARS-Cov-2 22073-22090:

GTCTCTCAGCCTTTTCTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22073-22090
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 323      GTCTCTCAGCCTTTTCTT 340
          || |||||||||||||||
Sbjct 828261    GTTCTCAGCCTTTTCTT 828244
```

3.1.220 NC_045512.2 SARS-Cov-2 5859-5874:

ATGTTTTCTACAAAGA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 5859-5874
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 109      ATGTTTTCTACAAAGA 124
          |||||||||||||||
Sbjct 1592533   ATGTTTTCTACAAAGA 1592518
```

3.1.221 NC_045512.2 SARS-Cov-2 17748-17763:

TGCTTGGAGAAAAGCT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17748-17763
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 948      TGCTTGGAGAAAAGCT 963
          |||||||||||||||
Sbjct 1117360   TGCTTGGAGAAAAGCT 1117345
```

3.1.222 NC_045512.2 SARS-Cov-2 17008-17023:

ATCTCAGATGAGTTTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17008-17023
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus
Query 258 ATCTCAGATGAGTTTT 273
          |||
Sbjct 1066836 ATCTCAGATGAGTTTT 1066851

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17004-17023
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 254 CAATATCTCAGATGAGTTTT 273
          ||| ||| |||
Sbjct 1802666 CAATGTCTGAGATGAGTTTT 1802647

```

3.1.223 NC_045512.2 SARS-Cov-2 730-744:

AGATTTTCAAGAAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 730-744
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 280 AGATTTTCAAGAAAA 294
          |||
Sbjct 399605 AGATTTTCAAGAAAA 399591

```

3.1.224 NC_045512.2 SARS-Cov-2 20407-20427:

TTTGAATTAGAAGATTTTATT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 20407-20427
Score = 34.6 bits (37), Expect = 0.15
Identities = 20/21 (95%), Gaps = 0/21 (0%)
Strand=Plus/Minus
Query 657 TTTGAATTAGAAGATTTTATT 677
          |||

```

Sbjct 1925416 TTTGAATTAGAAGATTCTATT 1925396

3.1.225 NC_045512.2 SARS-Cov-2 22118-22137:

TTCAAAAATCTTAGGGAATT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22118-22137
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 368      TTCAAAAATCTTAGGGAATT 387
          |||
Sbjct 943481  TTCAAAAATCTTGGGGATTT 943500
```

3.1.226 NC_045512.2 SARS-Cov-2 11848-11862:

AATGTCAGATGTAAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11848-11862
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 98      AATGTCAGATGTAAA 112
          |||
Sbjct 2071545  AATGTCAGATGTAAA 2071531
```

3.1.227 NC_045512.2 SARS-Cov-2 29775-29791:

TAGGGAGAGCTGCCTAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29775-29791
Score = 27.4 bits (29), Expect = 2.9
Identities = 16/17 (94%), Gaps = 0/17 (0%)
Strand=Plus/Minus
Query 25      TAGGGAGAGCTGCCTAT 41
          |||
Sbjct 2120766  TAGGGAGAGCTTCCTAT 2120750
```

3.1.228 NC_045512.2 SARS-Cov-2 21317-21339:

ATGGTTATGTCATGCATGCAAAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 21317-21339
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/23 (87%), Gaps = 0/23 (0%)
Strand=Plus/Plus
Query  567      ATGGTTATGTCATGCATGCAAAT  589
          ||| |||
Sbjct 1276130  ATGGTTATGTCATCGATGAAAAT 1276152
```

3.1.229 NC_045512.2 SARS-Cov-2 9702-9721:

TTTGTATTTCCACAAAGCAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 9702-9721
Score = 32.8 bits (35), Expect = 0.51
Identities = 19/20 (95%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query  952      TTTGTATTTCCACAAAGCAT  971
          ||| |||
Sbjct 1807383  TTTGTATTTCCACATAGCAT 1807402
```

3.1.230 NC_045512.2 SARS-Cov-2 25078-25095:

TAATGCTTCAGTTGTAAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 25078-25095
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query  328      TAATGCTTCAGTTGTAAA  345
          ||| |||
Sbjct 726890  TAATCTTCAGTTGTAAA  726873
```

3.1.231 NC_045512.2 SARS-Cov-2 19743-19762:

ATTGTTTGAATAAAACAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19743-19762
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query  943    ATTGTTTGAAAATAAAACAA  962
           ||| | |||||
Sbjct  78639  ATTTGTGAAAATAAAACAA  78620

```

3.1.232 NC_045512.2 SARS-Cov-2 8160-8193:

CTTTTATTTTCAGCAGCTCGGCAAGGGTTTGTTGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8160-8193
Score = 31.0 bits (33), Expect = 1.8
Identities = 27/34 (79%), Gaps = 0/34 (0%)
Strand=Plus/Plus
Query  410    CTTTATTTTCAGCAGCTCGGCAAGGGTTTGTTGA  443
           |||||
Sbjct  721659  CTTTATTTTCAGCAACTATGAAAGAGATTGATGA  721692

```

3.1.233 NC_045512.2 SARS-Cov-2 22803-22817:

AAACTGGAAAGATTG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22803-22817
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query  53      AAACTGGAAAGATTG  67
           |||||
Sbjct  1826775  AAACTGGAAAGATTG  1826789

```

3.1.234 NC_045512.2 SARS-Cov-2 15154-15174:

CATCAAA-AATTATTGAAATCA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15154-15174
Score = 31.0 bits (33), Expect = 1.8
Identities = 21/23 (91%), Gaps = 2/23 (9%)

```

```

Strand=Plus/Plus
Query  404      CATCAAA--AATTATTGAAATCA  424
          |||||  |||||
Sbjct  1859587  CATCAAAGTAATTATTGAAATCA  1859609

```

3.1.235 NC_045512.2 SARS-Cov-2 22392-22409:

TAAAATATAATGAAAATG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  22392-22409
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query  642      TAAAATATAATGAAAATG  659
          |||||  |||||
Sbjct  1834675  TAAAATATAATAAAAATG  1834658

```

3.1.236 NC_045512.2 SARS-Cov-2 9811-9830:

CTTTTTGTAAATAAAGAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  9811-9830
Score = 32.8 bits (35), Expect = 0.51
Identities = 19/20 (95%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query  61      CTTTTTGTAAATAAAGAAA  80
          || |||||
Sbjct  1107134  CTATTTGTAAATAAAGAAA  1107153

```

3.1.237 NC_045512.2 SARS-Cov-2 313-327:

CAGTTTGCCTGTTTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  313-327
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query  263      CAGTTTGCCTGTTTT  277
          |||||
Sbjct  1237363  CAGTTTGCCTGTTTT  1237349

```

3.1.238 NC_045512.2 SARS-Cov-2 1578-1593:

TTGTTGGAGAAGGTTC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1578-1593
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus
Query 828      TTGTTGGAGAAGGTTC 843
          |||
Sbjct 1152805  TTGTTGGAGAAGGTTC 1152820
```

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1576-1593
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 826      TGTGTTGGAGAAGGTTC 843
          |||
Sbjct 480797   TGTGTTGGAGCAGGTTC 480814
```

3.1.239 NC_045512.2 SARS-Cov-2 513-531:

ATGTTATGGTTGAGCTGGT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 513-531
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Plus
Query 63      ATGTTATGGTTGAGCTGGT 81
          |||
Sbjct 388324   ATGTTATGGTTGTGCTGGT 388342
```

3.1.240 NC_045512.2 SARS-Cov-2 6707-6725:

AAAGTTGTTAGTACAATA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 6707-6725
Score = 31.0 bits (33), Expect = 1.8
```

Identities = 18/19 (95%), Gaps = 0/19 (0%)
 Strand=Plus/Minus
 Query 957 AAAGTTGTTAGTACAACTA 975
 |||||
 Sbjct 1106976 AAAGTTGTTAGTATAACTA 1106958

3.1.241 NC_045512.2 SARS-Cov-2 26201-26216:

CTACTAGCGTGCCTTT

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 26201-26216
 Score = 30.1 bits (32), Expect = 1.8
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Minus
 Query 451 CTACTAGCGTGCCTTT 466
 |||||
 Sbjct 222382 CTACTAGCGTGCCTTT 222367

3.1.242 NC_045512.2 SARS-Cov-2 3258-3282:

AGACAACACTACTATTCAAACAATTGT

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 3258-3282
 Score = 28.3 bits (30), Expect = 6.2
 Identities = 21/25 (84%), Gaps = 0/25 (0%)
 Strand=Plus/Plus
 Query 508 AGACAACACTACTATTCAAACAATTGT 532
 |||| ||||| ||| |||
 Sbjct 909564 AGACGACTACTATTCAACCAAATGT 909588

3.1.243 NC_045512.2 SARS-Cov-2 29821-29836:

TTTAGTAGTGCTATCC

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 29821-29836
 Score = 25.6 bits (27), Expect = 6.3
 Identities = 15/16 (94%), Gaps = 0/16 (0%)
 Strand=Plus/Plus
 Query 21 TTTAGTAGTGCTATCC 36
 ||||| |||
 Sbjct 602440 TTTAGTAGTGCTGTCC 602455

3.1.244 NC_045512.2 SARS-Cov-2 26096-26115:

AAATTGTTGATGAGCCTGAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 26096-26115
Score = 29.2 bits (31), Expect = 6.2
Identities = 19/20 (95%), Gaps = 1/20 (5%)
Strand=Plus/Minus
Query 346      AAATTGTTGATGAGCCTGAA 365
          |||
Sbjct 206183  AAATTGTTGATGAG-CTGAA 206165
```

3.1.245 NC_045512.2 SARS-Cov-2 10067-10081:

AAAATGGCATTCCCA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 10067-10081
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 317      AAAATGGCATTCCCA 331
          |||
Sbjct 1571729  AAAATGGCATTCCCA 1571743
```

3.1.246 NC_045512.2 SARS-Cov-2 2236-2250:

TGAAATTGTCGGTGG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2236-2250
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 486      TGAAATTGTCGGTGG 500
          |||
Sbjct 1090534  TGAAATTGTCGGTGG 1090548
```

3.1.247 NC_045512.2 SARS-Cov-2 9784-9801:

TACTTTTGAAGAAGCTGC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 9784-9801
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 34          TACTTTTGAAGAAGCTGC 51
          || |||||
Sbjct 1203908 TATTTTGAAGAAGCTGC 1203891

```

3.1.248 NC_045512.2 SARS-Cov-2 27257-27274:

TGAGGACTTTTAAAGTTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 27257-27274
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 507          TGAGGACTTTTAAAGTTT 524
          |||||
Sbjct 1834149 TGAGGACTTTTAAAGCTT 1834132

```

3.1.249 NC_045512.2 SARS-Cov-2 29698-29717:

TTAGGGAGGACTTGAAAGAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29698-29717
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 948          TTAGGGAGGACTTGAAAGAG 967
          ||| |
Sbjct 1129481 TTATGAAGGACTTGAAAGAG 1129462

```

3.1.250 NC_045512.2 SARS-Cov-2 5104-5119:

TGAAGGTAAAACATTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 5104-5119
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)

```

```
Strand=Plus/Plus
Query 354      TGAAGGTAAAACATTT 369
          |||
Sbjct 726617  TGAAGGTAAAACATTT 726632
```

3.1.251 NC_045512.2 SARS-Cov-2 29306-29325:

AATTTCAAAGATCAAGTCAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29306-29325
Score = 32.8 bits (35), Expect = 0.51
Identities = 19/20 (95%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 556      AATTTCAAAGATCAAGTCAT 575
          |||
Sbjct 676371  AATTTCAAAGAGCAAGTCAT 676352
```

3.1.252 NC_045512.2 SARS-Cov-2 3168-3185:

CTCTTCAACCTGAAGAAG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3168-3185
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 418      CTCTTCAACCTGAAGAAG 435
          |||
Sbjct 167792  CTCTTAAACCTGAAGAAG 167775
```

3.1.253 NC_045512.2 SARS-Cov-2 17820-17839:

ACCAACTCAAACCTGTTGATT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17820-17839
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 70      ACCAACTCAAACCTGTTGATT 89
          |||
Sbjct 1694512  ACCAACTCAAACCTGACGATT 1694531
```

3.1.254 NC_045512.2 SARS-Cov-2 21818-21837:

TTTAATGATGGTGTTTATTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 21818-21837
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 68          TTTAATGATGGTGTTTATTT 87
          |||| |
Sbjct 1712903 TTTATTGATGGTGTTTT 1712884
```

3.1.255 NC_045512.2 SARS-Cov-2 4042-4064:

TAATGGCAATCTTCATCCAGATT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4042-4064
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/23 (87%), Gaps = 0/23 (0%)
Strand=Plus/Minus
Query 292        TAATGGCAATCTTCATCCAGATT 314
          || ||| || |
Sbjct 934350     TATTGAAACCTTCATCCAGATT 934328
```

3.1.256 NC_045512.2 SARS-Cov-2 8697-8714:

CTATTGATGGTGGTGTCA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8697-8714
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 947        CTATTGATGGTGGTGTCA 964
          || |
Sbjct 1228205 CTTTGGATGGTGGTGTCA 1228188
```

3.1.257 NC_045512.2 SARS-Cov-2 1605-1627:

ATGACAACCTTCTTGAATACTC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1605-1627
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/23 (87%), Gaps = 0/23 (0%)
Strand=Plus/Plus
Query 855      ATGACAACCTTCTTGAAATACTC 877
          ||| ||| ||| |||
Sbjct 903223  ATGACAACCTTTTCAAAAACCTC 903245

```

3.1.258 NC_045512.2 SARS-Cov-2 22957-22979:

GAGAGATATTTCAA—CTGAAATCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22957-22979
Score = 28.3 bits (30), Expect = 6.2
Identities = 22/26 (85%), Gaps = 3/26 (12%)
Strand=Plus/Plus
Query 207      GAGAGATATTTCAA---CTGAAATCT 229
          ||| ||| ||| ||| ||| |||
Sbjct 1568314  GAGAGATATTTCAAAATCTGAAAACCT 1568339

```

3.1.259 NC_045512.2 SARS-Cov-2 17258-17275:

AGTGTTTTGATAAATTCA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17258-17275
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 508      AGTGTTTTGATAAATTCA 525
          || ||| ||| ||| ||| |||
Sbjct 1317358  AGGGTTTTGATAAATTCA 1317375

```

3.1.260 NC_045512.2 SARS-Cov-2 23986-24000:

TCCATCAAAACCAAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23986-24000
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)

```

```

Strand=Plus/Minus
Query  986      TCCATCAAACCAAG  1000
          |||
Sbjct  302499  TCCATCAAACCAAG  302485

```

3.1.261 NC_045512.2 SARS-Cov-2 14587-14612:

GCTTCTGGTAATCTATTACTAGATAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  14587-14612
Score = 30.1 bits (32),  Expect = 1.8
Identities = 22/26 (85%), Gaps = 0/26 (0%)
Strand=Plus/Plus
Query  837      GCTTCTGGTAATCTATTACTAGATAA  862
          || |||
Sbjct  269358  GCCTCTGGTAATCTATCATTAGAAAA  269383

```

3.1.262 NC_045512.2 SARS-Cov-2 16971-16985:

CTATGTTAGAATTAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  16971-16985
Score = 28.3 bits (30),  Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query  221      CTATGTTAGAATTAC  235
          |||
Sbjct  1425413  CTATGTTAGAATTAC  1425399

```

3.1.263 NC_045512.2 SARS-Cov-2 28018-28032:

ATTCTAAATGGTATA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  28018-28032
Score = 28.3 bits (30),  Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query  268      ATTCTAAATGGTATA  282
          |||
Sbjct  1740216  ATTCTAAATGGTATA  1740202

```

3.1.264 NC_045512.2 SARS-Cov-2 13202-13220:

GAAGCCAATATGGATCAAG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13202-13220
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Plus
Query 452      GAAGCCAATATGGATCAAG 470
          |||
Sbjct 1007534  GAAGCCATTATGGATCAAG 1007552
```

3.1.265 NC_045512.2 SARS-Cov-2 12835-12850:

TTTGAAATGGGCTAGA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12835-12850
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 85      TTTGAAATGGGCTAGA 100
          |||
Sbjct 1331434  TTTGAAATGGGCTAGA 1331419
```

3.1.266 NC_045512.2 SARS-Cov-2 23323-23337:

TACACCATGTTCTTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23323-23337
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 573      TACACCATGTTCTTT 587
          |||
Sbjct 1458220  TACACCATGTTCTTT 1458234
```

3.1.267 NC_045512.2 SARS-Cov-2 19561-19575:

TTGTGGGTTTACAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19561-19575
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 811      TTGTGGGTTTACAAA 825
          |||
Sbjct 314870  TTGTGGGTTTACAAA 314856

```

3.1.268 NC_045512.2 SARS-Cov-2 27023-27038:

AATCACTGTTGCTACA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 27023-27038
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 273      AATCACTGTTGCTACA 288
          |||
Sbjct 105568  AATCACTGTTGCTACA 105553

```

3.1.269 NC_045512.2 SARS-Cov-2 6414-6428:

AAGTAGTGGAAAATC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 6414-6428
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 664      AAGTAGTGGAAAATC 678
          |||
Sbjct 793974  AAGTAGTGGAAAATC 793988

```

3.1.270 NC_045512.2 SARS-Cov-2 25089-25108:

TTGTAAACATTCAAAAAGAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 25089-25108
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)

```

```

Strand=Plus/Plus
Query 339      TTGTAACATTCAAAAAGAA 358
          ||||  |||
Sbjct 1513803  TTGTTACATTCAAAAAGAA 1513822

```

3.1.271 NC_045512.2 SARS-Cov-2 16501-16518:

GTTTTTGGTTTATATAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 16500-16518
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Plus
Query 750      AGTTTTTGGTTTATATAAA 768
          |||
Sbjct 702872   AGTTTTTGGTTTATATAAA 702890

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 16501-16518
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 1        GTTTTTGGTTTATATAAA 18
          |||
Sbjct 702873   GTTTTTGGTTTATATAAA 702890

```

3.1.272 NC_045512.2 SARS-Cov-2 6951-6966:

TTATAATTTGGTTTTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 6951-6966
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus
Query 201      TTATAATTTGGTTTTT 216
          |||
Sbjct 1691851  TTATAATTTGGTTTTT 1691866

```

3.1.273 NC_045512.2 SARS-Cov-2 23996-24010:

CCAAGCAAGAGGTCA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23996-24010
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 246 CCAAGCAAGAGGTCA 260
      |||
Sbjct 351621 CCAAGCAAGAGGTCA 351635
```

3.1.274 NC_045512.2 SARS-Cov-2 23618-23648:

AGTGTAGCTAGTCAATCCATCATTGCCTACA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23618-23648
Score = 28.3 bits (30), Expect = 6.2
Identities = 25/31 (81%), Gaps = 3/31 (10%)
Strand=Plus/Minus
Query 868 AGTGTAGCTAGTCAATCCATCATTGCCTACA 898
      |||
Sbjct 380858 AGTGTA---AGTCAATCCATCCTTGGATACA 380831
```

3.1.275 NC_045512.2 SARS-Cov-2 16537-16555:

GATAATGTTACTGACTTTA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 16537-16555
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Plus
Query 787 GATAATGTTACTGACTTTA 805
      |||
Sbjct 721757 GATAATATTACTGACTTTA 721775
```

3.1.276 NC_045512.2 SARS-Cov-2 881-908:

GCACGTGCTGGTAAAGCTTCATGCACTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 881-908
Score = 34.6 bits (37), Expect = 0.15
Identities = 25/28 (89%), Gaps = 1/28 (4%)
Strand=Plus/Minus
Query 131      GCACGTGCTGGTAAAGCTTCATGCACTT 158
          || ||||| ||||| |||||
Sbjct 2006821 GCTCGTGCTCGTAAAGCTTCA-GCACTT 2006795

```

3.1.277 NC_045512.2 SARS-Cov-2 19119-19136:

TTATAAAATAGAAGAATT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19119-19136
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 369      TTATAAAATAGAAGAATT 386
          || ||||| ||||| |||||
Sbjct 1888879 TTTATAAAATAGAAGAATT 1888862

```

3.1.278 NC_045512.2 SARS-Cov-2 29786-29799:

GCCTATATGGAAGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29786-29799
Score = 26.5 bits (28), Expect = 2.9
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus
Query 36      GCCTATATGGAAGA 49
          ||||| |||||
Sbjct 437409 GCCTATATGGAAGA 437422

```

3.1.279 NC_045512.2 SARS-Cov-2 5915-5931:

TTGGATGGTGTGTTGTTG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 5915-5931
Score = 31.9 bits (34), Expect = 0.51
Identities = 17/17 (100%), Gaps = 0/17 (0%)

```

```

Strand=Plus/Plus
Query 165      TTGGATGGTGTGTTGTTG 181
          |||
Sbjct 691171  TTGGATGGTGTGTTGTTG 691187

```

3.1.280 NC_045512.2 SARS-Cov-2 25399-25427:

TTGTTTATGAGAATCTTCACAA-TTGAAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 25399-25427
Score = 31.9 bits (34), Expect = 0.51
Identities = 26/31 (84%), Gaps = 2/31 (6%)
Strand=Plus/Plus
Query 649      TTGTTTATGAGAATCTTCACAA--TTGAAC 677
          |||
Sbjct 935084  TTGTTTATGAGGATGTTTCGCAAGTTTGAAC 935114

```

3.1.281 NC_045512.2 SARS-Cov-2 16528-16550:

GTTGGTAGCGATAATGTTACTGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 16528-16550
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/23 (87%), Gaps = 0/23 (0%)
Strand=Plus/Minus
Query 978      GTTGGTAGCGATAATGTTACTGA 1000
          |||
Sbjct 1498616  GTTGGTAGCGAAATTGTTTCTGA 1498594

```

3.1.282 NC_045512.2 SARS-Cov-2 19820-19844:

CAGAGGTGAAAATACTCAATAATTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19820-19844
Score = 28.3 bits (30), Expect = 6.2
Identities = 21/25 (84%), Gaps = 0/25 (0%)
Strand=Plus/Plus
Query 70      CAGAGGTGAAAATACTCAATAATTT 94
          ||
Sbjct 493241  CAAAGGTGAAAATAGACAAGAATTT 493265

```

3.1.283 NC_045512.2 SARS-Cov-2 28847-28865:

AACAGTTCAAGAAATTCAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 28847-28865
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Minus
Query 97 AACAGTTCAAGAAATTCAA 115
      |||
Sbjct 1586605 AACAGTTCAAGAAAGTCAA 1586587
```

3.1.284 NC_045512.2 SARS-Cov-2 1881-1895:

AGGCTGCTCGTGTTG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1881-1895
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 131 AGGCTGCTCGTGTTG 145
      |||
Sbjct 21973 AGGCTGCTCGTGTTG 21987
```

3.1.285 NC_045512.2 SARS-Cov-2 20251-20265:

ATTGATTTCTTAGAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 20251-20265
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 501 ATTGATTTCTTAGAA 515
      |||
Sbjct 278293 ATTGATTTCTTAGAA 278307
```

3.1.286 NC_045512.2 SARS-Cov-2 23120-23134:

GCACCAGCAACTGTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23120-23134
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 370      GCACCAGCAACTGTT 384
          |||
Sbjct 1974294 GCACCAGCAACTGTT 1974308

```

3.1.287 NC_045512.2 SARS-Cov-2 15804-15821:

TCAAAACAATGTTTTTAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15804-15821
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 54      TCAAAACAATGTTTTTAT 71
          |||
Sbjct 1690427 TCAAAACAATGTTTTGAT 1690410

```

3.1.288 NC_045512.2 SARS-Cov-2 29718-29731:

CCACCACATTTTCA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29718-29731
Score = 26.5 bits (28), Expect = 9.5
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Minus
Query 268     CCACCACATTTTCA 281
          |||
Sbjct 933667  CCACCACATTTTCA 933654

```

3.1.289 NC_045512.2 SARS-Cov-2 11135-11150:

TTTGCAATGATGTTTG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11135-11150
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)

```

```

Strand=Plus/Minus
Query 385      TTTGCAATGATGTTT 400
          |||
Sbjct 2129864 TTTGCAATGATGTTT 2129849

```

3.1.290 NC_045512.2 SARS-Cov-2 15733-15750:

TGTTTCAATAGCACTTAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15733-15750
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 983      TGTTTCAATAGCACTTAT 1000
          |||
Sbjct 971150   TGTTTCAATAGCATTAT 971167

```

3.1.291 NC_045512.2 SARS-Cov-2 3016-3036:

TTCACATATGTATTGTTCTTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3016-3036
Score = 34.6 bits (37), Expect = 0.15
Identities = 20/21 (95%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 266      TTCACATATGTATTGTTCTTT 286
          |||
Sbjct 693726   TTCACATATATATTGTTCTTT 693746

```

3.1.292 NC_045512.2 SARS-Cov-2 19120-19135:

TATAAAATAGAAGAAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19120-19135
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 370      TATAAAATAGAAGAAT 385
          |||
Sbjct 1030042   TATAAAATAGAAGAAT 1030027

```

3.1.293 NC_045512.2 SARS-Cov-2 8471-8490:

AATAACTTACCTTTTAAGTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8471-8490
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 721      AATAACTTACCTTTTAAGTT 740
          ||||| | |||||
Sbjct 1526911 AATAAGTGACCTTTTAAGTT 1526930
```

3.1.294 NC_045512.2 SARS-Cov-2 9612-9626:

TTACTAATGATGTTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 9612-9626
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 862      TTACTAATGATGTTT 876
          |||||
Sbjct 1209801 TTACTAATGATGTTT 1209815
```

3.1.295 NC_045512.2 SARS-Cov-2 11683-11702:

GACTCTTGGTGTTTATGATT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11683-11702
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 933      GACTCTTGGTGTTTATGATT 952
          ||||| |||||
Sbjct 1859908 GACTCTTGGTGTAATGATT 1859927
```

3.1.296 NC_045512.2 SARS-Cov-2 29110-29129:

AGAACAAACCCAAGGAAATT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29110-29129
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 360      AGAACAAACCCAAGGAAATT 379
          ||| |||| |||||
Sbjct 921945  AGACCAAAGCCAAGGAAATT 921926

```

3.1.297 NC_045512.2 SARS-Cov-2 17264-17278:

TTGATAAATTCAAAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17264-17278
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 514      TTGATAAATTCAAAG 528
          |||||
Sbjct 2009184  TTGATAAATTCAAAG 2009170

```

3.1.298 NC_045512.2 SARS-Cov-2 19125-19144:

AATAGAAGAATTATTCTATT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19125-19144
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 375      AATAGAAGAATTATTCTATT 394
          |||| |||||
Sbjct 8816      AATAAAAGAATTATTCAATT 8797

```

3.1.299 NC_045512.2 SARS-Cov-2 15622-15641:

TATGAGTGTCTCTATAGAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15622-15641
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)

```

```

Strand=Plus/Plus
Query  872      TATGAGTGTCTCTATAGAAA  891
          ||||| ||||| ||||| ||
Sbjct  178856    TATGAATGTCTCTATAGGAA  178875

```

3.1.300 NC_045512.2 SARS-Cov-2 13687-13701:

GAAGAAACAATTTAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  13681-13701
Score = 30.1 bits (32),  Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query  931      CAACATGAAGAAACAATTTAT  951
          || ||||| ||||| |||||
Sbjct  2131483  CATCATGAAAAACAATTTAT  2131503

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  13687-13701
Score = 28.3 bits (30),  Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query  937      GAAGAAACAATTTAT  951
          ||||| ||||| |||||
Sbjct  374060    GAAGAAACAATTTAT  374074

```

3.1.301 NC_045512.2 SARS-Cov-2 10054-10071:

GAGTGGTTTTAGAAAAAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  10054-10071
Score = 29.2 bits (31),  Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query  304      GAGTGGTTTTAGAAAAAT  321
          ||||| ||||| |||||
Sbjct  1393992  GAGTGATTTTAGAAAAAT  1394009

```

3.1.302 NC_045512.2 SARS-Cov-2 19933-19948:

ACTGACATAGCCAAGA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19933-19948
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 183      ACTGACATAGCCAAGA 198
          |||
Sbjct 185052  ACTGACATAGCCAAGA 185037
```

3.1.303 NC_045512.2 SARS-Cov-2 10110-10127:

AAGTAACTTGTGGTACAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 10110-10127
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 360      AAGTAACTTGTGGTACAA 377
          |||
Sbjct 1658597  AAGTAATTTGTGGTACAA 1658580
```

3.1.304 NC_045512.2 SARS-Cov-2 22145-22180:

AAGAATATTGATG-GTTATTTTAAAATATATTCTAAG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22145-22180
Score = 32.8 bits (35), Expect = 0.51
Identities = 30/37 (81%), Gaps = 1/37 (3%)
Strand=Plus/Minus
Query 395      AAGAATATTGATG-GTTATTTTAAAATATATTCTAAG 430
          |||
Sbjct 1807011  AAGAATTTTGACATGTTCTTTTAAAATATAGTCCAAG 1806975
```

3.1.305 NC_045512.2 SARS-Cov-2 25945-25964:

CAGATTGGTGGTTATACTGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 25945-25964
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 195      CAGATTGGTGGTTATACTGA 214
          || ||||||||||||| |||
Sbjct 1318698  CAAATTGGTGGTTATAGTGA 1318679

```

3.1.306 NC_045512.2 SARS-Cov-2 880-897:

AGCACGTGCTGGTAAAGC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 880-897
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 130      AGCACGTGCTGGTAAAGC 147
          ||||| |||||||||||||
Sbjct 1466699  AGCACTTGCTGGTAAAGC 1466716

```

3.1.307 NC_045512.2 SARS-Cov-2 24673-24687:

AAAAAGAGTTGATTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 24673-24687
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 923      AAAAAGAGTTGATTT 937
          |||||||||||||||
Sbjct 606373  AAAAAGAGTTGATTT 606359

```

3.1.308 NC_045512.2 SARS-Cov-2 3804-3825:

AAAATCTCTATGACAAACTTGT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3804-3825
Score = 31.9 bits (34), Expect = 0.51
Identities = 20/22 (91%), Gaps = 0/22 (0%)

```

```

Strand=Plus/Plus
Query  54      AAAATCTCTATGACAAACTTGT  75
          ||| | | | | | | | | | | | | | | |
Sbjct 1071730 AAAATCTCTATGAGAAACTGGT 1071751

```

3.1.309 NC_045512.2 SARS-Cov-2 584-598:

CTTGTCCCTCATGTG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  584-598
Score = 28.3 bits (30),  Expect = 6.2
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Plus
Query  134      CTTGTCCCTCATGTG  148
          ||| | | | | | | | | | | |
Sbjct 2112181 CTTGTCCCTCATGTG  2112195

```

3.1.310 NC_045512.2 SARS-Cov-2 13884-13906:

ATACAATTGTTGTGATGATGATT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  13884-13906
Score = 33.7 bits (36),  Expect = 0.15
  Identities = 21/23 (91%), Gaps = 0/23 (0%)
  Strand=Plus/Minus
Query  134      ATACAATTGTTGTGATGATGATT  156
          ||| | | | | | | | | | | | | | |
Sbjct 1733187 ATACAATTGTTCTGATGATTATT  1733165

```

3.1.311 NC_045512.2 SARS-Cov-2 4768-4782:

TATTGAAACCATCTC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  4768-4782
Score = 28.3 bits (30),  Expect = 6.2
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Plus
Query  18      TATTGAAACCATCTC  32
          ||| | | | | | | | | | | |
Sbjct 1044979 TATTGAAACCATCTC  1044993

```

3.1.312 NC_045512.2 SARS-Cov-2 16884-16902:

TTACAAATTAAATGTTGGT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 16884-16902
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Plus
Query 134      TTACAAATTAAATGTTGGT 152
          ||| |||||
Sbjct 369856  TTAAAAATTAAATGTTGGT 369874
```

3.1.313 NC_045512.2 SARS-Cov-2 24353-24369:

ATTGGCAAATTC AAGA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 24353-24369
Score = 31.9 bits (34), Expect = 0.51
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus
Query 603      ATTGGCAAATTC AAGA 619
          |||||
Sbjct 527277  ATTGGCAAATTC AAGA 527261
```

3.1.314 NC_045512.2 SARS-Cov-2 15143-15167:

ATAGACAGTTTCATCAAAAATTATT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15143-15167
Score = 29.2 bits (31), Expect = 6.2
Identities = 22/25 (88%), Gaps = 1/25 (4%)
Strand=Plus/Minus
Query 393      ATAGACAGTTTCATCAAAAATTATT 417
          ||||| | ||||| |||||
Sbjct 569967  ATAGATAATTCATC-AAAATTATT 569944
```

3.1.315 NC_045512.2 SARS-Cov-2 2299-2316:

CTTTAAGCTTGTAATAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2299-2316
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 549      CTTTAAGCTTGTAATAA 566
          |||
Sbjct 1370469 CTTTAAGCTTGTAATAA 1370452

```

3.1.316 NC_045512.2 SARS-Cov-2 17336-17356:

CAGCAGATATAGTTGTCTTTG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17336-17356
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 586      CAGCAGATATAGTTGTCTTTG 606
          ||| |||| |||
Sbjct 848888   CAGAAGATACAGTTGTCTTTG 848908

```

3.1.317 NC_045512.2 SARS-Cov-2 7828-7852:

TGTTAACTTAGACAACCTGAGAGCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7828-7852
Score = 28.3 bits (30), Expect = 6.2
Identities = 21/25 (84%), Gaps = 0/25 (0%)
Strand=Plus/Minus
Query 78      TGTTAACTTAGACAACCTGAGAGCT 102
          || || |||
Sbjct 734347   TGGTAGCTTAGACAACCTGCTAGCT 734323

```

3.1.318 NC_045512.2 SARS-Cov-2 1576-1590:

TGTTGTTGGAGAAGG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1576-1590
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)

```

```

Strand=Plus/Plus
Query  826      TGGTGTGGAGAAGG  840
          |||||
Sbjct  1062494  TGGTGTGGAGAAGG  1062508

```

3.1.319 NC_045512.2 SARS-Cov-2 26424-26451:

TCGTGTAAAAATCTGAATTCTTCTAGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query  = NC_045512.2 SARS-Cov-2  26424-26451
Score  = 30.1 bits (32),  Expect  = 1.8
Identities  = 24/28 (86%),  Gaps  = 1/28 (4%)
Strand=Plus/Plus
Query  674      TCGTGTAAAAATCTGAATTCTTCTAGA  701
          |||||
Sbjct  697914  TCGTGTAAAAATC-GTATGATTCTAGA  697940

```

3.1.320 NC_045512.2 SARS-Cov-2 23389-23407:

TGTTCTTTATCAGGATGTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query  = NC_045512.2 SARS-Cov-2  23389-23407
Score  = 31.0 bits (33),  Expect  = 1.8
Identities  = 18/19 (95%),  Gaps  = 0/19 (0%)
Strand=Plus/Minus
Query  639      TGTTCTTTATCAGGATGTT  657
          |||  |||||
Sbjct  2039039  TGTTTTTTATCAGGATGTT  2039021

```

3.1.321 NC_045512.2 SARS-Cov-2 26643-26664:

AACAGGAATAGGTTTTTGTATA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query  = NC_045512.2 SARS-Cov-2  26643-26664
Score  = 28.3 bits (30),  Expect  = 6.2
Identities  = 20/22 (91%),  Gaps  = 1/22 (5%)
Strand=Plus/Minus
Query  893      AACAGGAATAGGTTTTTGTATA  914
          |||  |||||
Sbjct  1381994  AACAG-AATAGGTTTTTGTGTA  1381974

```

3.1.322 NC_045512.2 SARS-Cov-2 1128-1148:

TTGAAAAGAAAAAGCTTGATG

```
> NZ_CP020550.1 Streptococcus pneumoniae strain Hu17 plasmid pSpn_Hu17
Length=6012
Query = NC_045512.2 SARS-Cov-2 1128-1148
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 378 TTGAAAAGAAAAAGCTTGATG 398
          |||
Sbjct 2782 TTGAAAAGAAAAAGCAAGATG 2802
```

3.1.323 NC_045512.2 SARS-Cov-2 12855-12872:

CTAAGAGTGATGGAAGTGG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12855-12872
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 105 CTAAGAGTGATGGAAGTGG 122
          |||
Sbjct 1198112 CTAAGATTGATGGAAGTGG 1198095
```

3.1.324 NC_045512.2 SARS-Cov-2 2110-2128:

CATCTTTGGCACTGTTTAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2110-2128
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Plus
Query 360 CATCTTTGGCACTGTTTAT 378
          |||
Sbjct 585020 CATCTTTGGCACTGTCTAT 585038
```

3.1.325 NC_045512.2 SARS-Cov-2 13153-13168:

GATGTTGTGTACACAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13153-13168
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus
Query 403      GATGTTGTGTACACAC 418
          |||
Sbjct 665855  GATGTTGTGTACACAC 665870

```

3.1.326 NC_045512.2 SARS-Cov-2 4867-4881:

TGTATATTACACTAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4867-4881
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 117      TGTATATTACACTAG 131
          |||
Sbjct 1968735  TGTATATTACACTAG 1968749

```

3.1.327 NC_045512.2 SARS-Cov-2 21720-21742:

ACTTGTTCTTACCTTTCTTTTCC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 21720-21742
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/23 (87%), Gaps = 0/23 (0%)
Strand=Plus/Minus
Query 970      ACTTGTTCTTACCTTTCTTTTCC 992
          || ||| || |||
Sbjct 240861  ACCTGTTTCATAGCTTTCTTTTCC 240839

```

3.1.328 NC_045512.2 SARS-Cov-2 4090-4104:

CATCACTTTCTTAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4090-4104
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)

```

```

Strand=Plus/Plus
Query  340      CATCACTTTCTTAAA  354
          |||
Sbjct  1392819  CATCACTTTCTTAAA  1392833

```

3.1.329 NC_045512.2 SARS-Cov-2 26166-26180:

AGTAATGGAACCAAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 26166-26180
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query  416      AGTAATGGAACCAAT  430
          |||
Sbjct  2111533  AGTAATGGAACCAAT  2111547

```

3.1.330 NC_045512.2 SARS-Cov-2 24475-24503:

TGCAATTTCAAGTGTTTTAAATGATATCC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 24475-24503
Score = 31.0 bits (33), Expect = 1.8
Identities = 24/29 (83%), Gaps = 0/29 (0%)
Strand=Plus/Minus
Query  725      TGCAATTTCAAGTGTTTTAAATGATATCC  753
          ||| || ||| |||
Sbjct  820987  TGCAATTTCAACGGTTTCAATTGATTTC  820959

```

3.1.331 NC_045512.2 SARS-Cov-2 29529-29542:

CCTAAACTCATGCA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29529-29542
Score = 26.5 bits (28), Expect = 9.5
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Minus
Query  79      CCTAAACTCATGCA  92
          |||
Sbjct  692861  CCTAAACTCATGCA  692848

```

3.1.332 NC_045512.2 SARS-Cov-2 15411-15442:

TGAGTGTGCTCAAGTATTGAGTGAAATGGTCA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15411-15442
Score = 31.9 bits (34), Expect = 0.51
Identities = 26/32 (81%), Gaps = 0/32 (0%)
Strand=Plus/Minus
Query 661 TGAGTGTGCTCAAGTATTGAGTGAAATGGTCA 692
      ||| | | | | | | | | | | | | |
Sbjct 203740 TGAGTGTGCACAAGGAGCTATTGAAATGGTCA 203709

```

3.1.333 NC_045512.2 SARS-Cov-2 4352-4374:

GAGAAGCAAGAAATTCTTGAAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4352-4374
Score = 30.1 bits (32), Expect = 1.8
Identities = 21/23 (91%), Gaps = 1/23 (4%)
Strand=Plus/Plus
Query 602 GAGAAGCAAGAAATTCTTGAAC 624
      ||| | | | | | | | | | || ||||
Sbjct 190189 GAGAAGCAAGAAA-TCGTGAAC 190210

```

3.1.334 NC_045512.2 SARS-Cov-2 7246-7266:

GTTTTTGGCATATATTCTTTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7246-7266
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 496 GTTTTTGGCATATATTCTTTT 516
      ||||| | | | | | | | |
Sbjct 1208687 GTTTTGTTATATATTCTTTT 1208707

```

3.1.335 NC_045512.2 SARS-Cov-2 14850-14871:

ATTTGTAGTTGAAGTTGTTGAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 14850-14871
Score = 31.9 bits (34), Expect = 0.51
Identities = 20/22 (91%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query 100      AATTGTAGTTGAAGTTGTTGAT 121
          ||||| ||||| ||||| |||||
Sbjct 1422021  AATTGCAGTTGAAGTTGCTGAT 1422042

```

3.1.336 NC_045512.2 SARS-Cov-2 7616-7630:

AATTGTGTTAATTGT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7616-7630
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 866      AATTGTGTTAATTGT 880
          ||||| ||||| ||||| |||||
Sbjct 2001936  AATTGTGTTAATTGT 2001950

```

3.1.337 NC_045512.2 SARS-Cov-2 1018-1032:

GCAGACACCTTTTGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1018-1032
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 268      GCAGACACCTTTTGA 282
          ||||| ||||| ||||| |||||
Sbjct 415011   GCAGACACCTTTTGA 414997

```

3.1.338 NC_045512.2 SARS-Cov-2 28870-28890:

AGGCAGCAGTAGGGGAACTTC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 28870-28890
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)

```

```

Strand=Plus/Plus
Query 120    AGGCAGCAGTAGGGGAAGCTTC 140
          |||
Sbjct 15188  AGGCAGCAGTAGGGAATCTTC 15208

```

3.1.339 NC_045512.2 SARS-Cov-2 11563-11580:

CCCTATTTTCTTCATAAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11563-11580
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 813    CCCTATTTTCTTCATAAC 830
          |||
Sbjct 1697269  CCAATTTTCTTCATAAC 1697286

```

3.1.340 NC_045512.2 SARS-Cov-2 19750-19764:

GAAAATAAAACAACA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19750-19764
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 950    GAAAATAAAACAACA 964
          |||
Sbjct 968013  GAAAATAAAACAACA 968027

```

3.1.341 NC_045512.2 SARS-Cov-2 26792-26810:

GATGTGGCTCAGCTACTTC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 26792-26810
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Minus
Query 42     GATGTGGCTCAGCTACTTC 60
          ||
Sbjct 968101  GAGGTGGCTCAGCTACTTC 968083

```

3.1.342 NC_045512.2 SARS-Cov-2 24475-24499:

TGCAATTTCAAGTGTTTTAAATGAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 24475-24499
Score = 28.3 bits (30), Expect = 6.2
Identities = 21/25 (84%), Gaps = 0/25 (0%)
Strand=Plus/Minus
Query 975      TGCAATTTCAAGTGTTTTAAATGAT 999
          ||| | | | | | | | | | | | | | | | | | | | | |
Sbjct 820987  TGCAATTTCAACGGTTTCAATTGAT 820963
```

3.1.343 NC_045512.2 SARS-Cov-2 4022-4036:

TTGTTACTTTATATT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4022-4036
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 272      TTGTTACTTTATATT 286
          ||| | | | | | | | | | | | | | | | | | | | | |
Sbjct 663482  TTGTTACTTTATATT 663468
```

3.1.344 NC_045512.2 SARS-Cov-2 9625-9644:

TTCTTTTTTTAGCACATATTC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 9625-9644
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 875      TTCTTTTTTTAGCACATATTC 894
          ||| | | | | | | | | | | | | | | | | | | | | |
Sbjct 1199240  TTCTCCTTTAGCACATATTC 1199259
```

3.1.345 NC_045512.2 SARS-Cov-2 5057-5071:

TATTTGGATGGAGCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 5057-5071
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 307      TATTGGATGGAGCT 321
          |||
Sbjct 1569013 TATTGGATGGAGCT 1568999

```

3.1.346 NC_045512.2 SARS-Cov-2 7133-7150:

GTTTGTCTTAGTGGTTTA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7133-7150
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 383      GTTTGTCTTAGTGGTTTA 400
          ||| |||
Sbjct 1734181 GTTTTCTTAGTGGTTTA 1734164

```

3.1.347 NC_045512.2 SARS-Cov-2 4783-4805:

ACTTGCTGGTTCCTATAAAGATT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4783-4805
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/23 (87%), Gaps = 0/23 (0%)
Strand=Plus/Minus
Query 33      ACTTGCTGGTTCCTATAAAGATT 55
          ||| ||| | |||
Sbjct 353784 ACTTGCTGGTTCGAGAAAGATT 353762

```

3.1.348 NC_045512.2 SARS-Cov-2 7008-7022:

CTGCTTTAGGTGTTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7008-7022
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)

```

```
Strand=Plus/Plus
Query 258      CTGCTTTAGGTGTTT 272
          |||
Sbjct 100209   CTGCTTTAGGTGTTT 100223
```

3.1.349 NC_045512.2 SARS-Cov-2 8268-8285:

ATAGTTGTAATAACTATA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8268-8285
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 518      ATAGTTGTAATAACTATA 535
          |||
Sbjct 108933   ATAGTTGTAATAACAATA 108950
```

3.1.350 NC_045512.2 SARS-Cov-2 9937-9954:

TAGCTACAGAGAAGCTGC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 9937-9954
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 187      TAGCTACAGAGAAGCTGC 204
          |||
Sbjct 786760   TAGCTCCAGAGAAGCTGC 786743
```

3.1.351 NC_045512.2 SARS-Cov-2 26793-26817:

ATGTGGCTCAGCTACTTCATTGCTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 26793-26817
Score = 28.3 bits (30), Expect = 6.2
Identities = 21/25 (84%), Gaps = 0/25 (0%)
Strand=Plus/Minus
Query 43       ATGTGGCTCAGCTACTTCATTGCTT 67
          ||
Sbjct 2029699   ATATGGCTCAGCTACTGCAATGATT 2029675
```

3.1.352 NC_045512.2 SARS-Cov-2 2948-2965:

ATTGATTTAGATGAGTGG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2948-2965
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 198      ATTGATTTAGATGAGTGG 215
          ||| |||
Sbjct 1086134  ATTTATTTAGATGAGTGG 1086151
```

3.1.353 NC_045512.2 SARS-Cov-2 8102-8122:

GTTGCAACTGCAGAAGCTGAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8102-8122
Score = 39.2 bits (42), Expect = 0.003
Identities = 21/21 (100%), Gaps = 0/21 (0%)
Strand=Plus/Minus
Query 352      GTTGCAACTGCAGAAGCTGAA 372
          |||
Sbjct 1306817  GTTGCAACTGCAGAAGCTGAA 1306797
```

3.1.354 NC_045512.2 SARS-Cov-2 3793-3817:

TGTCTTTGATAAAAATCTCTATGAC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3793-3817
Score = 28.3 bits (30), Expect = 6.2
Identities = 21/25 (84%), Gaps = 0/25 (0%)
Strand=Plus/Minus
Query 43      TGTCTTTGATAAAAATCTCTATGAC 67
          ||| |||
Sbjct 698836  TGTCTATGATAAAAATCCTTATAAC 698812
```

3.1.355 NC_045512.2 SARS-Cov-2 12775-12794:

TTACTACAACACAACAAAGG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12775-12794
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 25      TTACTACAACACAACAAAGG 44
          |||| | |||||
Sbjct 880430  TTACGAAAACACAACAAAGG 880411

```

3.1.356 NC_045512.2 SARS-Cov-2 21103-21130:

TTTTTCACTTACATTTGTGGGTTTATAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 21103-21130
Score = 30.1 bits (32), Expect = 1.8
Identities = 24/28 (86%), Gaps = 1/28 (4%)
Strand=Plus/Minus
Query 353      TTTTCACTTACATTTGTGGGTTTATAC 380
          ||||| ||||| ||| || | |||||
Sbjct 210730  TTTTCACTTACTTTTTTGAG-TTATAC 210704

```

3.1.357 NC_045512.2 SARS-Cov-2 5073-5087:

ATGTTACTAAAATAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 5073-5087
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 323      ATGTTACTAAAATAA 337
          |||||
Sbjct 2102088  ATGTTACTAAAATAA 2102102

```

3.1.358 NC_045512.2 SARS-Cov-2 26424-26450:

TCGTGTAAAAATCTGAATTCTTCTAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 26424-26450
Score = 28.3 bits (30), Expect = 6.2
Identities = 23/27 (85%), Gaps = 1/27 (4%)

```

```

Strand=Plus/Plus
Query 974      TCGTGTAAAAAATCTGAATTCTTCTAG 1000
          ||| ||| ||| ||| ||| |||
Sbjct 697914   TCGTGTAAAAAATC-GTATGATTCTAG 697939

```

3.1.359 NC_045512.2 SARS-Cov-2 9985-10005:

CTTCAGTAACTCAGGTTCTGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 9985-10005
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 235      CTTCAGTAACTCAGGTTCTGA 255
          ||| ||| ||| ||| ||| |||
Sbjct 13113    CTTTAGTATCTCAGGTTCTGA 13133

```

3.1.360 NC_045512.2 SARS-Cov-2 15204-15218:

AATTGGAACAAGCAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15204-15218
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 454      AATTGGAACAAGCAA 468
          ||| ||| ||| ||| ||| |||
Sbjct 1456338  AATTGGAACAAGCAA 1456324

```

3.1.361 NC_045512.2 SARS-Cov-2 24052-24077:

TGCTGGCTTCATCAAACAATATGGTG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 24052-24077
Score = 34.6 bits (37), Expect = 0.15
Identities = 23/26 (88%), Gaps = 0/26 (0%)
Strand=Plus/Plus
Query 302      TGCTGGCTTCATCAAACAATATGGTG 327
          ||| ||| | || ||| ||| ||| |||
Sbjct 964122   TGCTGGCATTATGAAACAATATGGTG 964147

```

3.1.362 NC_045512.2 SARS-Cov-2 16833-16847:

CTTTGAAAAAGGTGA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 16833-16847
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 83      CTTTGAAAAAGGTGA 97
          |||
Sbjct 788128  CTTTGAAAAAGGTGA 788142
```

3.1.363 NC_045512.2 SARS-Cov-2 23176-23193:

TGTCAATTTCAACTTCAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23176-23193
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 426     TGTCAATTTCAACTTCAA 443
          ||| |||
Sbjct 20656   TGTCTATTTCAACTTCAA 20639
```

3.1.364 NC_045512.2 SARS-Cov-2 17004-17023:

CAATATCTCAGATGAGTTTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17004-17023
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 254     CAATATCTCAGATGAGTTTT 273
          ||| |||
Sbjct 1802666 CAATGTCTGAGATGAGTTTT 1802647
```

3.1.365 NC_045512.2 SARS-Cov-2 8104-8119:

TGCAACTGCAGAAGCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8104-8119
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 354      TGCAACTGCAGAAGCT 369
          |||
Sbjct 735251  TGCAACTGCAGAAGCT 735236

```

3.1.366 NC_045512.2 SARS-Cov-2 24878-24892:

CAAAGGAATTTTAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 24878-24892
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 128      CAAAGGAATTTTAT 142
          |||
Sbjct 1903843  CAAAGGAATTTTAT 1903829

```

3.1.367 NC_045512.2 SARS-Cov-2 17263-17283:

TTTGATAAATTCAAAGTGAAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17263-17283
Score = 34.6 bits (37), Expect = 0.15
Identities = 20/21 (95%), Gaps = 0/21 (0%)
Strand=Plus/Minus
Query 513      TTTGATAAATTCAAAGTGAAT 533
          |||
Sbjct 457711  TTTGATAAATTCAAAGTGGAT 457691

```

3.1.368 NC_045512.2 SARS-Cov-2 10600-10617:

TGGACCTTTTGTTGACAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 10600-10617
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)

```

```

Strand=Plus/Plus
Query  850      TGGACCTTTTGTGACAG  867
          || |||||
Sbjct  1818892  TGCACCTTTTGTGACAG  1818909

```

3.1.369 NC_045512.2 SARS-Cov-2 2676-2690:

CTAATATGATGGTAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2676-2690
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query  926      CTAATATGATGGTAA  940
          |||||
Sbjct  1870932  CTAATATGATGGTAA  1870946

```

3.1.370 NC_045512.2 SARS-Cov-2 18557-18593:

CACTTAAAAATCTCTCTGACAGAGTCGTATTTGTCTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 18557-18593
Score = 37.4 bits (40), Expect = 0.012
Identities = 31/37 (84%), Gaps = 1/37 (3%)
Strand=Plus/Minus
Query  807      CACTTAAAAATCTCTCTGACAGAGTCGTATTTGTCTT  843
          ||||| | |||| | |||| | |||||
Sbjct  590600  CACTTAAAA-TATCTTTACAGAAGTGTATTTGTCTT  590565

```

3.1.371 NC_045512.2 SARS-Cov-2 27694-27713:

TTTCTTATTGTTGCGGCAAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 27694-27713
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query  944      TTTCTTATTGTTGCGGCAAT  963
          ||||| | ||||
Sbjct  74398  TTTCTTATTGTTTCAGCAAT  74417

```

3.1.372 NC_045512.2 SARS-Cov-2 7490-7510:

TGTATGATGTGTTACAAACGT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7490-7510
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Minus
Query 740      TGTATGATGTGTTACAAACGT 760
          |||||  |||||  |||||  ||
Sbjct 961359  TGTATGTTGTGTTACAAATGT 961339
```

3.1.373 NC_045512.2 SARS-Cov-2 29112-29133:

AACAAACCCAAGGAAATTTTGG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29112-29133
Score = 32.8 bits (35), Expect = 0.51
Identities = 21/22 (95%), Gaps = 1/22 (5%)
Strand=Plus/Plus
Query 362      AACAAACCCAAGGAAATTTTGG 383
          |||||  |||||  |||||  |||||
Sbjct 932989  AACAAACCCAA-GAAATTTTGG 933009
```

3.1.374 NC_045512.2 SARS-Cov-2 8296-8310:

TAACAAAGTTGAAAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8296-8310
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 546      TAACAAAGTTGAAAA 560
          |||||  |||||  |||||  |||||
Sbjct 2125999  TAACAAAGTTGAAAA 2126013
```

3.1.375 NC_045512.2 SARS-Cov-2 25961-25981:

CTGAAAAAATGGGAATCTGGAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 25961-25981
Score = 34.6 bits (37), Expect = 0.15
Identities = 20/21 (95%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 211      CTGAAAAATGGAATCTGGAG 231
          |||
Sbjct 938744  CTGAAAAATGGAATCTGGAG 938764

```

3.1.376 NC_045512.2 SARS-Cov-2 7822-7852:

TCATTTTGTTAACCTT-AGACAACCTGAGAGCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7822-7852
Score = 32.8 bits (35), Expect = 0.51
Identities = 27/32 (84%), Gaps = 1/32 (3%)
Strand=Plus/Minus
Query 72      TCATTTTGTTAACCTT-AGACAACCTGAGAGCT 102
          ||| | |||| | | |||
Sbjct 1165848 TCAGTCTGTTATCTTTAGACAACCTGAGCGCT 1165817

```

3.1.377 NC_045512.2 SARS-Cov-2 29419-29444:

ACCGCAGAGACAGAAGAAACAGCAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29419-29444
Score = 30.1 bits (32), Expect = 1.8
Identities = 22/26 (85%), Gaps = 0/26 (0%)
Strand=Plus/Minus
Query 669      ACCGCAGAGACAGAAGAAACAGCAAA 694
          ||| | ||| |||
Sbjct 546880  ACCCCTGAGCCAGAAGAAACAGCGAA 546855

```

3.1.378 NC_045512.2 SARS-Cov-2 17754-17773:

GAGAAAAGCTGTCTTTATTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17754-17773
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)

```

```

Strand=Plus/Minus
Query  4      GAGAAAAGCTGTCTTTATTT  23
          |||||
Sbjct  375428  GAGAAAAGCTGACGTTATTT  375409

```

3.1.379 NC_045512.2 SARS-Cov-2 16927-16941:

ACAGTAATGCCATTA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 16927-16941
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query  177      ACAGTAATGCCATTA  191
          |||||
Sbjct  1910838  ACAGTAATGCCATTA  1910852

```

3.1.380 NC_045512.2 SARS-Cov-2 27100-27119:

TTGCTGCATACAGTCGCTAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 27100-27119
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query  350      TTGCTGCATACAGTCGCTAC  369
          |||||
Sbjct  769180  TTGCTGCATACAGTTGCCAC  769161

```

3.1.381 NC_045512.2 SARS-Cov-2 11448-11478:

ATCAAGCCATTTCCATGTGGGCTCTTATAAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11448-11478
Score = 36.5 bits (39), Expect = 0.042
Identities = 27/31 (87%), Gaps = 2/31 (6%)
Strand=Plus/Plus
Query  698      ATCAAGCCATTTCCATGTGGGCTCTTATAAT  728
          |||||
Sbjct  1109570  ATCAAGCCATTGCCA--TGGTCTCTTATAAT  1109598

```

3.1.382 NC_045512.2 SARS-Cov-2 23909-23928:

GCACAAGTCAAACAAATTTA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23909-23928
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 159      GCACAAGTCAAACAAATTTA 178
          |||| | |||||
Sbjct 1300034 GCACGAATCAAACAAATTTA 1300015
```

3.1.383 NC_045512.2 SARS-Cov-2 24712-24727:

GTCCTTCCCTCAGTCA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 24700-24727
Score = 31.0 bits (33), Expect = 1.8
Identities = 24/28 (86%), Gaps = 2/28 (7%)
Strand=Plus/Minus
Query 950      CTATCATCTTATGTCCTTCCCTCAGTCA 977
          ||||| | | |||||
Sbjct 680592 CTATCAGC--AAGTCCTTCCCTCAGTCA 680567
```

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 24712-24727
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 12      GTCCTTCCCTCAGTCA 27
          |||||
Sbjct 680582 GTCCTTCCCTCAGTCA 680567
```

3.1.384 NC_045512.2 SARS-Cov-2 21946-21966:

TAAAGTCTGTGAATTTCAATT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 21946-21966
Score = 30.1 bits (32), Expect = 1.8
```

Identities = 19/21 (90%), Gaps = 0/21 (0%)
 Strand=Plus/Minus
 Query 196 TAAAGTCTGTGAATTTCAATT 216
 |||| |||||
 Sbjct 1806507 TAAAATCTGTGAATTTCACTT 1806487

3.1.385 NC_045512.2 SARS-Cov-2 23428-23443:

TGCTATTCATGCAGAT

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 23428-23443
 Score = 30.1 bits (32), Expect = 1.8
 Identities = 16/16 (100%), Gaps = 0/16 (0%)
 Strand=Plus/Minus
 Query 678 TGCTATTCATGCAGAT 693
 |||||
 Sbjct 1471747 TGCTATTCATGCAGAT 1471732

3.1.386 NC_045512.2 SARS-Cov-2 8239-8256:

ACATCAATCTGACATAGA

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 8239-8256
 Score = 29.2 bits (31), Expect = 6.2
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Minus
 Query 489 ACATCAATCTGACATAGA 506
 |||||
 Sbjct 955042 ACATCAATCTGACAGAGA 955025

3.1.387 NC_045512.2 SARS-Cov-2 29806-29823:

ATGTGTAAAATTAATTTT

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 29806-29823
 Score = 29.2 bits (31), Expect = 0.84
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Minus
 Query 56 ATGTGTAAAATTAATTTT 73
 || |||||
 Sbjct 1731941 ATTTGTAAAATTAATTTT 1731924

3.1.388 NC_045512.2 SARS-Cov-2 19878-19897:

GGACTACAAAAGAGATGCTC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19878-19897
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 128      GGACTACAAAAGAGATGCTC 147
          ||||| ||||| ||||| ||
Sbjct 555936   GGACTGCAAAAAGAGATGATC 555917
```

3.1.389 NC_045512.2 SARS-Cov-2 1266-1280:

GCGATTTTGTTAAAG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1266-1280
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 516      GCGATTTTGTTAAAG 530
          ||||| ||||| ||||| ||
Sbjct 1392379   GCGATTTTGTTAAAG 1392365
```

3.1.390 NC_045512.2 SARS-Cov-2 29855-29874:

TTCTTAGGAGAATGACaaaa

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29855-29874
Score = 23.8 bits (25), Expect = 8.9
Identities = 17/20 (85%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 5      TTCTTAGGAGAATGACaaaa 24
          ||||| ||||| ||| ||
Sbjct 1592423   TTCTTAGGAGAAAAACATAA 1592404
```

3.1.391 NC_045512.2 SARS-Cov-2 969-986:

AGCATGAAATTGCTTGGT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 969-986
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 219      AGCATGAAATTGCTTGGT 236
            |||
Sbjct 1216855  AGCATGAAATTGTTGGT 1216872

```

3.1.392 NC_045512.2 SARS-Cov-2 28948-28978:

CAGATTGAACCAGCTTGAGAGCAAAATGTCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 28948-28978
Score = 31.0 bits (33), Expect = 1.8
Identities = 26/31 (84%), Gaps = 1/31 (3%)
Strand=Plus/Plus
Query 198      CAGATTGAACCAGCTTGAGAGCAAAATGTCT 228
            |||
Sbjct 1424304  CAGAT-GAACCAGCTTGAGCTCCTAATGTCT 1424333

```

3.1.393 NC_045512.2 SARS-Cov-2 19003-19023:

TTAG-CAGACAAATTCCCAGTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 18999-19023
Score = 31.0 bits (33), Expect = 1.8
Identities = 23/26 (88%), Gaps = 1/26 (4%)
Strand=Plus/Plus
Query 249      ATTATTAG-CAGACAAATTCCCAGTT 273
            |||
Sbjct 1052883  ATTTTATAGACAGAAAATTCCCAGTT 1052908

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19003-19023
Score = 28.3 bits (30), Expect = 6.2
Identities = 20/22 (91%), Gaps = 1/22 (5%)
Strand=Plus/Plus
Query 3        TTAG-CAGACAAATTCCCAGTT 23
            |||

```

Sbjct 1052887 TTAGACAGAAAAATTCCAGTT 1052908

3.1.394 NC_045512.2 SARS-Cov-2 6402-6416:

CAGTCTCTGAAGAAG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 6402-6416
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 652      CAGTCTCTGAAGAAG 666
          |||
Sbjct 1601643 CAGTCTCTGAAGAAG 1601657
```

3.1.395 NC_045512.2 SARS-Cov-2 22687-22702:

CACTTTTAAGTGTTAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22687-22702
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus
Query 937      CACTTTTAAGTGTTAT 952
          |||
Sbjct 1018406 CACTTTTAAGTGTTAT 1018421
```

3.1.396 NC_045512.2 SARS-Cov-2 12211-12237:

GTCTTTGAATGTGGCTAAATCTGAATT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12211-12237
Score = 32.8 bits (35), Expect = 0.51
Identities = 24/27 (89%), Gaps = 1/27 (4%)
Strand=Plus/Plus
Query 461      GTCTTTGAATGTGGCTAAATCTGAATT 487
          ||| ||||| ||| |||
Sbjct 65571      GTCCTTGAA-GTGCCTAAATCTGAATT 65596
```

3.1.397 NC_045512.2 SARS-Cov-2 8765-8779:

TTTGACACATGGTTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8765-8779
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 15          TTTGACACATGGTTT 29
          |||
Sbjct 1432800    TTTGACACATGGTTT 1432786
```

3.1.398 NC_045512.2 SARS-Cov-2 1576-1593:

TGTTGTTGGAGAAGGTTTC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1576-1593
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 826          TGTTGTTGGAGAAGGTTTC 843
          |||
Sbjct 480797      TGTTGTTGGAGCAGGTTTC 480814
```

3.1.399 NC_045512.2 SARS-Cov-2 23093-23112:

GTAGTACTTTCTTTTGAACT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23093-23112
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 343          GTAGTACTTTCTTTTGAACT 362
          |||
Sbjct 812152      GTAGTACTTTCTTATAAACT 812133
```

3.1.400 NC_045512.2 SARS-Cov-2 21060-21078:

TAAGACTAAAAATG-TTACA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 21060-21078
Score = 29.2 bits (31), Expect = 6.2
Identities = 19/20 (95%), Gaps = 1/20 (5%)
Strand=Plus/Plus
Query 310 TAAGACTAAAAATG-TTACA 328
      |||
Sbjct 512978 TAAGACTAAAAATGATTACA 512997

```

3.1.401 NC_045512.2 SARS-Cov-2 9622-9638:

TGTTTCTTTTTTAGCAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 9622-9638
Score = 31.9 bits (34), Expect = 0.51
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus
Query 872 TGTTTCTTTTTTAGCAC 888
      |||
Sbjct 463603 TGTTTCTTTTTTAGCAC 463619

```

3.1.402 NC_045512.2 SARS-Cov-2 20724-20740:

AGAAAAGTGTGACCTTC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 20724-20740
Score = 31.9 bits (34), Expect = 0.51
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus
Query 974 AGAAAAGTGTGACCTTC 990
      |||
Sbjct 1006801 AGAAAAGTGTGACCTTC 1006817

```

3.1.403 NC_045512.2 SARS-Cov-2 29324-29341:

ATTTTGCTGAATAAGCAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29324-29341
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)

```

```

Strand=Plus/Plus
Query  574      ATTTTGCTGAATAAGCAT  591
          |||
Sbjct  216694  ATTTTGCTGAATAAACAT  216711

```

3.1.404 NC_045512.2 SARS-Cov-2 962-989:

GAACATGAGCATGAAAT-TGCTTGGTACA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 962-989
Score = 30.1 bits (32), Expect = 1.8
Identities = 25/30 (83%), Gaps = 2/30 (7%)
Strand=Plus/Plus
Query  212      GAACATGAGCATGAAAT--TGCTTGGTACA  239
          |||
Sbjct  550063  GAACATGAGCAAGAAATCATGTCTGGTACA  550092

```

3.1.405 NC_045512.2 SARS-Cov-2 15871-15893:

GAATTTTGCTCTCAACATACAAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15871-15893
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/23 (87%), Gaps = 0/23 (0%)
Strand=Plus/Plus
Query  121      GAATTTTGCTCTCAACATACAAT  143
          ||
Sbjct  1802126  GATTTTACTCTCAACATAAAAT  1802148

```

3.1.406 NC_045512.2 SARS-Cov-2 21865-21879:

AAGAGGCTGGATTTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 21865-21879
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query  115      AAGAGGCTGGATTTT  129
          |||
Sbjct  706636  AAGAGGCTGGATTTT  706622

```

3.1.407 NC_045512.2 SARS-Cov-2 1760-1775:

TTCAAACAAATTGTTG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1760-1775
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 10          TTCAAACAAATTGTTG 25
          |||
Sbjct 1926670    TTCAAACAAATTGTTG 1926655
```

3.1.408 NC_045512.2 SARS-Cov-2 20002-20019:

GATGGTCAAGTAGACTTA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 20002-20019
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 252          GATGGTCAAGTAGACTTA 269
          |||
Sbjct 1165448    GATGGTCAAGTAGAATTA 1165431
```

3.1.409 NC_045512.2 SARS-Cov-2 19338-19358:

AAGTGCTTTTGTTAATTTAAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19338-19358
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 588          AAGTGCTTTTGTTAATTTAAA 608
          |||
Sbjct 538735    AAGTGCTTTTGTGATTTTAAA 538755
```

3.1.410 NC_045512.2 SARS-Cov-2 22002-22020:

AAAACAACAAAAGTTGGAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22002-22020
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Plus
Query 252      AAAACAACAAAAGTTGGAT 270
          |||
Sbjct 1075716 AAAACAACAAAAGTTGGAT 1075734

```

3.1.411 NC_045512.2 SARS-Cov-2 8776-8796:

GTTTAGCCAGCGTGGTGGTAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8776-8796
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Minus
Query 26      GTTTAGCCAGCGTGGTGGTAG 46
          |||
Sbjct 1841405 GTTTAGCCAGCATTGTGGTAG 1841385

```

3.1.412 NC_045512.2 SARS-Cov-2 3668-3682:

TATGAAAATTTTAAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3668-3682
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 918     TATGAAAATTTTAAT 932
          |||
Sbjct 596145  TATGAAAATTTTAAT 596159

```

3.1.413 NC_045512.2 SARS-Cov-2 17853-17868:

AGAATATGACTATGTC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17853-17868
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)

```

```

Strand=Plus/Plus
Query 103      AGAATATGACTATGTC 118
          |||
Sbjct 1050500  AGAATATGACTATGTC 1050515

```

3.1.414 NC_045512.2 SARS-Cov-2 20049-20081:

TACAGAAGGTAGTGTTAAAGGTTTACAACCATC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 20049-20081
Score = 29.2 bits (31), Expect = 6.2
Identities = 26/33 (79%), Gaps = 0/33 (0%)
Strand=Plus/Plus
Query 299      TACAGAAGGTAGTGTTAAAGGTTTACAACCATC 331
          |||
Sbjct 2063005  TACAGAAGGTACTTTTAAAGATAACAAACCATC 2063037

```

3.1.415 NC_045512.2 SARS-Cov-2 23160-23174:

TGGTTAAAAACAAAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23160-23174
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 410      TGGTTAAAAACAAAT 424
          |||
Sbjct 400065   TGGTTAAAAACAAAT 400079

```

3.1.416 NC_045512.2 SARS-Cov-2 22744-22758:

TGTCTATGCAGATTC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22744-22758
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 944      TGTCTATGCAGATTC 958
          |||
Sbjct 10432    TGTCTATGCAGATTC 10446

```

3.1.417 NC_045512.2 SARS-Cov-2 13054-13071:

TTCAACTGTATTATCTTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13054-13071
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 304      TTCAACTGTATTATCTTT 321
          |||
Sbjct 1005657 TTCAACTGTATTATTTT 1005640
```

3.1.418 NC_045512.2 SARS-Cov-2 27943-27961:

ACCAAGAATGTAGTTTACA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 27943-27961
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Plus
Query 193      ACCAAGAATGTAGTTTACA 211
          |||
Sbjct 1690984 ACCAAGGATGTAGTTTACA 1691002
```

3.1.419 NC_045512.2 SARS-Cov-2 26662-26680:

ATATAATTAAGTTAATTTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 26662-26680
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Plus
Query 912      ATATAATTAAGTTAATTTT 930
          |||
Sbjct 175496   ATAGAATTAAGTTAATTTT 175514
```

3.1.420 NC_045512.2 SARS-Cov-2 25441-25461:

CAAGG-TGAAATCAAGGATGCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 25441-25461
Score = 28.3 bits (30), Expect = 6.2
Identities = 20/22 (91%), Gaps = 1/22 (5%)
Strand=Plus/Minus
Query 691 CAAGG-TGAAATCAAGGATGCT 711
      ||||| | |||||
Sbjct 1029587 CAAGGATAAAATCAAGGATGCT 1029566

```

3.1.421 NC_045512.2 SARS-Cov-2 1337-1360:

GGTTA-CTTACCCCAAATGCTGTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1337-1360
Score = 29.2 bits (31), Expect = 6.2
Identities = 22/25 (88%), Gaps = 1/25 (4%)
Strand=Plus/Minus
Query 587 GGTTA-CTTACCCCAAATGCTGTT 610
      ||||| |||| | |||||
Sbjct 1680346 GGTATCTTAGCTCAAATGCTGTT 1680322

```

3.1.422 NC_045512.2 SARS-Cov-2 17256-17270:

AGAGTGTTTTGATAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17256-17270
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 506 AGAGTGTTTTGATAA 520
      |||||
Sbjct 1984915 AGAGTGTTTTGATAA 1984901

```

3.1.423 NC_045512.2 SARS-Cov-2 18664-18700:

CTATGTGATAGACGTGCCACATGCTTTTCCACTGCTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 18664-18700
Score = 29.2 bits (31), Expect = 6.2
Identities = 29/37 (78%), Gaps = 2/37 (5%)

```

Strand=Plus/Minus
Query 914 CTATGTGATAGACGTGCCACATGCTTTTCCACTGCTT 950
|| ||||| |||| | |||||
Sbjct 647382 CTCTGTGATAGACGTTCCAC--GCTTGTTATCTGCTT 647348

3.1.424 NC_045512.2 SARS-Cov-2 2371-2385:

CTTGAATTTAGGTGA

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2371-2385
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 621 CTTGAATTTAGGTGA 635
|||||
Sbjct 1790524 CTTGAATTTAGGTGA 1790510

3.1.425 NC_045512.2 SARS-Cov-2 2496-2510:

GAGAAACACTTCCCA

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2496-2510
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 746 GAGAAACACTTCCCA 760
|||||
Sbjct 1303651 GAGAAACACTTCCCA 1303637

3.1.426 NC_045512.2 SARS-Cov-2 22262-22296:

AACATCACTAGGTTTCAAACCTTT--ACTTGCTTTACA

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22262-22296
Score = 29.2 bits (31), Expect = 6.2
Identities = 29/37 (78%), Gaps = 2/37 (5%)
Strand=Plus/Minus
Query 512 AACATCACTAGGTTTCAAACCTTT--ACTTGCTTTACA 546
||| || | | | |||| |||| | |||||
Sbjct 802062 AACTTCTCAAAGCTTCAATCTTTTACTTGCTTTACA 802026

3.1.427 NC_045512.2 SARS-Cov-2 19941-19960:

AGCCAAGAAACCAACTGAAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19941-19960
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 191      AGCCAAGAAACCAACTGAAA 210
          || |||
Sbjct 316073  AGTCAAGAAACCAACTGCAA 316054
```

3.1.428 NC_045512.2 SARS-Cov-2 1800-1819:

CAAAAGGAAAAGCTAAAAAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1800-1819
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 50      CAAAAGGAAAAGCTAAAAAA 69
          |||
Sbjct 669364  CAAAAGGAAAAGCAAATAA 669345
```

3.1.429 NC_045512.2 SARS-Cov-2 12857-12871:

AAGAGTGATGGAACT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12857-12871
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 107     AAGAGTGATGGAACT 121
          |||
Sbjct 1554428 AAGAGTGATGGAACT 1554414
```

3.1.430 NC_045512.2 SARS-Cov-2 17662-17676:

TATAAGGGTGTTATC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17662-17676
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query  912      TATAAGGGTGTTC  926
          |||
Sbjct 1838166 TATAAGGGTGTTC 1838152

```

3.1.431 NC_045512.2 SARS-Cov-2 23000-23014:

TGTAATGGTGTGAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23000-23014
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query  250      TGTAATGGTGTGAA  264
          |||
Sbjct 1054027 TGTAATGGTGTGAA 1054013

```

3.1.432 NC_045512.2 SARS-Cov-2 9396-9411:

CAGCATCTATAGTAGC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 9396-9411
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus
Query  646      CAGCATCTATAGTAGC  661
          |||
Sbjct 1123138 CAGCATCTATAGTAGC 1123153

```

3.1.433 NC_045512.2 SARS-Cov-2 22057-22072:

TTGCACTTTTGAATAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22057-22072
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)

```

```

Strand=Plus/Minus
Query 307      TTGCACTTTTGAATAT 322
          |||
Sbjct 346172  TTGCACTTTTGAATAT 346157

```

3.1.434 NC_045512.2 SARS-Cov-2 1807-1821:

AAAAGCTAAAAAAGG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1807-1821
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 57      AAAAGCTAAAAAAGG 71
          |||
Sbjct 2053809 AAAAGCTAAAAAAGG 2053823

```

3.1.435 NC_045512.2 SARS-Cov-2 23717-23740:

ACTATTAGTGTTACCACAGAAATT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23717-23740
Score = 31.0 bits (33), Expect = 1.8
Identities = 21/24 (88%), Gaps = 0/24 (0%)
Strand=Plus/Plus
Query 967      ACTATTAGTGTTACCACAGAAATT 990
          ||| |||| | |||
Sbjct 1115188  ACTTTTAGTATAACCACAGAAATT 1115211

```

3.1.436 NC_045512.2 SARS-Cov-2 8372-8392:

GTAGCAAAAAGTCACAACATT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 8372-8392
Score = 31.0 bits (33), Expect = 1.8
Identities = 20/21 (95%), Gaps = 1/21 (5%)
Strand=Plus/Minus
Query 622      GTAGCAAAAAGTCACAACATT 642
          ||| |||
Sbjct 367188  GTAG-AAAAGTCACAACATT 367169

```

3.1.437 NC_045512.2 SARS-Cov-2 2570-2587:

CCTACTAGTGAAGCTGTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2570-2587
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 820      CCTACTAGTGAAGCTGTT 837
          ||| |||
Sbjct 1917499 CCTTCTAGTGAAGCTGTT 1917516
```

3.1.438 NC_045512.2 SARS-Cov-2 17963-17982:

TGTCTGATAGAGACC-TTTAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17963-17982
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/22 (91%), Gaps = 2/22 (9%)
Strand=Plus/Minus
Query 213      TGTCTGATAGAGACC--TTTAT 232
          |||
Sbjct 1527647 TGTCTGATAGAGACCAATTTAT 1527626
```

3.1.439 NC_045512.2 SARS-Cov-2 3193-3212:

AGAAGATTGGTTAGATGATG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3193-3212
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 443      AGAAGATTGGTTAGATGATG 462
          |||
Sbjct 995083  AGAAGAATTGTTAGATGATG 995102
```

3.1.440 NC_045512.2 SARS-Cov-2 14851-14871:

TTTGTAGTTGAAGTTGTTGAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 14850-14871
Score = 31.9 bits (34), Expect = 0.51
Identities = 20/22 (91%), Gaps = 0/22 (0%)
Strand=Plus/Plus
Query 100      ATTGTAGTTGAAGTTGTTGAT 121
          ||||| ||||| ||||| |||||
Sbjct 1422021  ATTGCAGTTGAAGTTGCTGAT 1422042

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 14851-14871
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 1        TTTGTAGTTGAAGTTGTTGAT 21
          |||| | ||||| ||||| ||||
Sbjct 1422022  TTTGCAGTTGAAGTTGCTGAT 1422042

```

3.1.441 NC_045512.2 SARS-Cov-2 6610-6649:

AGTATTAGGT-TTGAAAACCCTTGCTACTCATG-GTTTAGCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 6610-6649
Score = 34.6 bits (37), Expect = 0.15
Identities = 35/42 (83%), Gaps = 3/42 (7%)
Strand=Plus/Minus
Query 860      AGTATTAGGT-TTGAAAACCCTTGCTACTCATG-GTTTAGCT 899
          ||||| | || | ||||| ||||| |||| | || | |||| | ||
Sbjct 869932   AGTATCAAGTGTGAAAACCCTTGATACT-ATGCGTTTTGCT 869892

```

3.1.442 NC_045512.2 SARS-Cov-2 2807-2827:

AGGATTGATAAAGTACTTAAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2807-2827
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Minus
Query 57      AGGATTGATAAAGTACTTAAT 77
          ||| | ||||| ||||| |||||

```

Sbjct 1300354 AGGGTGGATAAAGTACTTAAT 1300334

3.1.443 NC_045512.2 SARS-Cov-2 13094-13113:

GCTAAAGCTTACAAAGATTA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13094-13113
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 344      GCTAAAGCTTACAAAGATTA 363
          ||||| ||||| ||
Sbjct 1935274 GCTAAAGCTTATAAAGAATA 1935255
```

3.1.444 NC_045512.2 SARS-Cov-2 27667-27681:

GAAGTTCAAGAACTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 27667-27681
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 917      GAAGTTCAAGAACTT 931
          ||||| ||||| ||||| ||||| |||||
Sbjct 1142835 GAAGTTCAAGAACTT 1142849
```

3.1.445 NC_045512.2 SARS-Cov-2 26422-26441:

TCTCGTGTAAAAATCTGAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 26422-26441
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 672      TCTCGTGTAAAAATCTGAA 691
          ||| ||||| ||||| ||||| ||
Sbjct 237314 TCTTGTGTAAAAATCTTAA 237295
```

3.1.446 NC_045512.2 SARS-Cov-2 3716-3742:

GCTGGTATTTTTGGTGCTGACCCTATA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3716-3742
Score = 32.8 bits (35), Expect = 0.51
Identities = 24/27 (89%), Gaps = 1/27 (4%)
Strand=Plus/Minus
Query 966      GCTGGTATTTTTGGTGCTGACCCTATA 992
          ||||| ||||| ||||| ||||| ||||| ||
Sbjct 1512962  GCTGG-ATTTTTGGTGCTGCCCTTTA 1512937
```

3.1.447 NC_045512.2 SARS-Cov-2 24205-24231:

AATCACTTCTGGTTGGACCTTTGGTGC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 24205-24231
Score = 31.9 bits (34), Expect = 0.51
Identities = 23/27 (85%), Gaps = 0/27 (0%)
Strand=Plus/Plus
Query 455      AATCACTTCTGGTTGGACCTTTGGTGC 481
          ||||| ||||| ||||| ||||| ||||| ||
Sbjct 770232  AATCACTTCTGGTTTGACAAATGGTGC 770258
```

3.1.448 NC_045512.2 SARS-Cov-2 14855-14870:

TAGTTGAAGTTGTTGA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 14855-14870
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus
Query 105      TAGTTGAAGTTGTTGA 120
          ||||| ||||| ||||| ||||| ||||| ||
Sbjct 12965  TAGTTGAAGTTGTTGA 12980
```

3.1.449 NC_045512.2 SARS-Cov-2 12571-12587:

AGATGCAGATAGTAAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12571-12587
Score = 31.9 bits (34), Expect = 0.51
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus
Query 821      AGATGCAGATAGTAAAA 837
          |||
Sbjct 362768  AGATGCAGATAGTAAAA 362784

```

3.1.450 NC_045512.2 SARS-Cov-2 4321-4337:

CTTTTACATTCTACCAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4321-4337
Score = 31.9 bits (34), Expect = 0.51
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Plus
Query 571      CTTTTACATTCTACCAT 587
          |||
Sbjct 1650276  CTTTTACATTCTACCAT 1650292

```

3.1.451 NC_045512.2 SARS-Cov-2 4527-4541:

GATTTTACTTTTACA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4527-4541
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 777      GATTTTACTTTTACA 791
          |||
Sbjct 1093429  GATTTTACTTTTACA 1093415

```

3.1.452 NC_045512.2 SARS-Cov-2 16855-16885:

GATGCTGTTGTTTACCGAGGTACAACAACCTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 16855-16885
Score = 30.1 bits (32), Expect = 1.8
Identities = 25/31 (81%), Gaps = 0/31 (0%)

```

```

Strand=Plus/Plus
Query 105      GATGCTGTTGTTTACCGAGGTACAACAACCTT 135
          |||| | |||| | | | | |||||
Sbjct 1632159  GATGATGTTGGTAAGCCAAGTACAACAACCTT 1632189

```

3.1.453 NC_045512.2 SARS-Cov-2 15695-15712:

ATTTCTCAATGATGATAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15695-15712
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 945      ATTTCTCAATGATGATAC 962
          |||||
Sbjct 1198632  ATTTCTCAATGATGACAC 1198649

```

3.1.454 NC_045512.2 SARS-Cov-2 26094-26109:

TAAAATTGTTGATGAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 26094-26109
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 344      TAAAATTGTTGATGAG 359
          |||||
Sbjct 1754940  TAAAATTGTTGATGAG 1754925

```

3.1.455 NC_045512.2 SARS-Cov-2 12333-12349:

CAAAAGTTACTAGTGCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12333-12349
Score = 31.9 bits (34), Expect = 0.51
Identities = 17/17 (100%), Gaps = 0/17 (0%)
Strand=Plus/Minus
Query 583      CAAAAGTTACTAGTGCT 599
          |||||
Sbjct 1782012  CAAAAGTTACTAGTGCT 1781996

```

3.1.456 NC_045512.2 SARS-Cov-2 13929-13950:

TGATTTTGTAGAAAACCCAGAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13929-13950
Score = 28.3 bits (30), Expect = 6.2
Identities = 20/22 (91%), Gaps = 1/22 (5%)
Strand=Plus/Minus
Query 179      TGATTTTGTAGAAAACCCAGAT 200
          |||
Sbjct 1825403 TGATTTTGTAGAACACCAGAT 1825383
```

3.1.457 NC_045512.2 SARS-Cov-2 14680-14705:

AATTTTAACAAAGACTTCTATGACTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 14680-14705
Score = 30.1 bits (32), Expect = 1.8
Identities = 22/26 (85%), Gaps = 0/26 (0%)
Strand=Plus/Minus
Query 930      AATTTTAACAAAGACTTCTATGACTT 955
          || |||
Sbjct 524419   AAATTTGACAAAGACTTCTTTGATTT 524394
```

3.1.458 NC_045512.2 SARS-Cov-2 5632-5646:

TGGTAAACAAGCTAC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 5632-5646
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 882      TGGTAAACAAGCTAC 896
          |||
Sbjct 811175   TGGTAAACAAGCTAC 811189
```

3.1.459 NC_045512.2 SARS-Cov-2 24700-24727:

CTATCATCTTATGTCCTTCCCTCAGTCA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 24700-24727
Score = 31.0 bits (33), Expect = 1.8
Identities = 24/28 (86%), Gaps = 2/28 (7%)
Strand=Plus/Minus
Query 950      CTATCATCTTATGTCCTTCCCTCAGTCA 977
          ||||| | | |||
Sbjct 680592  CTATCAGC--AAGTCCTTCCCTCAGTCA 680567

```

3.1.460 NC_045512.2 SARS-Cov-2 2051-2068:

GTTGTAATGGCCTACATT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2051-2068
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 301      GTTGTAATGGCCTACATT 318
          |||
Sbjct 370897  GTTGTAATGGCCTATATT 370914

```

3.1.461 NC_045512.2 SARS-Cov-2 9782-9797:

AGTACTTTTGAAGAAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 9782-9797
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 32      AGTACTTTTGAAGAAG 47
          |||
Sbjct 1590054  AGTACTTTTGAAGAAG 1590039

```

3.1.462 NC_045512.2 SARS-Cov-2 13805-13819:

ACACAATGGCAGACC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13805-13819
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)

```

```

Strand=Plus/Minus
Query  55      ACACAATGGCAGACC  69
          |||
Sbjct  1648496 ACACAATGGCAGACC  1648482

```

3.1.463 NC_045512.2 SARS-Cov-2 14917-14932:

GTCATCGTCAACAACC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 14917-14932
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus
Query  167      GTCATCGTCAACAACC  182
          |||
Sbjct  674997   GTCATCGTCAACAACC  675012

```

3.1.464 NC_045512.2 SARS-Cov-2 1702-1716:

TTTTTCTGCTTCCAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1702-1716
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query  952      TTTTCTGCTTCCAC  966
          |||
Sbjct  1884997   TTTTCTGCTTCCAC  1885011

```

3.1.465 NC_045512.2 SARS-Cov-2 6396-6410:

TAAAACCAGTCTCTG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 6396-6410
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query  646      TAAAACCAGTCTCTG  660
          |||
Sbjct  621474   TAAAACCAGTCTCTG  621460

```

3.1.466 NC_045512.2 SARS-Cov-2 3204-3224:

TAGATGATGATAGTCAACAAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3204-3224
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 454 TAGATGATGATAGTCAACAAA 474
      |||
Sbjct 729870 TAGATGATGATTGGCAACAAA 729890
```

3.1.467 NC_045512.2 SARS-Cov-2 4333-4359:

ACCATCTATTATCTCTAATGAG-AAGCA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4333-4359
Score = 30.1 bits (32), Expect = 1.8
Identities = 24/28 (86%), Gaps = 1/28 (4%)
Strand=Plus/Minus
Query 583 ACCATCTATTATCTCTAATGAG-AAGCA 609
      |||
Sbjct 894697 ACCATCTATTA ACTCTTTT GAGTAAGCA 894670
```

3.1.468 NC_045512.2 SARS-Cov-2 6691-6705:

TAAGCCTTTTCTTAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 6691-6705
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 941 TAAGCCTTTTCTTAA 955
      |||
Sbjct 882189 TAAGCCTTTTCTTAA 882175
```

3.1.469 NC_045512.2 SARS-Cov-2 7271-7290:

AGGTTTTTCTATGTA CTTGG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7271-7290
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 521      AGGTTTTTCTATGTA CTGG 540
          |||
Sbjct 1468240 AGGTTTTTCTATTTATTTGG 1468259

```

3.1.470 NC_045512.2 SARS-Cov-2 10450-10464:

CAATTTCACTATTAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 10450-10464
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 700      CAATTTCACTATTAA 714
          |||
Sbjct 1803753 CAATTTCACTATTAA 1803767

```

3.1.471 NC_045512.2 SARS-Cov-2 22987-23006:

CGGTAGCACACCTTGTAATG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22987-23006
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 237      CGGTAGCACACCTTGTAATG 256
          |||
Sbjct 105991   CGGTGGGACACCTTGTAATG 106010

```

3.1.472 NC_045512.2 SARS-Cov-2 1673-1692:

AATGAAGAGATCGCCATTAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1673-1692
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)

```

```

Strand=Plus/Plus
Query  923      AATGAAGAGATCGCCATTAT  942
          |||
Sbjct  1843544  AATGAAGAGATCTCCAATAT  1843563

```

3.1.473 NC_045512.2 SARS-Cov-2 23965-23979:

TTTTTCACAAATATT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  23965-23979
Score = 28.3 bits (30),  Expect = 6.2
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Plus
Query  215      TTTTTCACAAATATT  229
          |||
Sbjct  969555  TTTTTCACAAATATT  969569

```

3.1.474 NC_045512.2 SARS-Cov-2 17362-17376:

ATTTCAATGGCCACA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  17362-17376
Score = 28.3 bits (30),  Expect = 6.2
  Identities = 15/15 (100%), Gaps = 0/15 (0%)
  Strand=Plus/Plus
Query  612      ATTTCAATGGCCACA  626
          |||
Sbjct  1523298  ATTTCAATGGCCACA  1523312

```

3.1.475 NC_045512.2 SARS-Cov-2 9412-9437:

TGGTGGTATTGTAGCTATCGTAGTAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2  9412-9437
Score = 30.1 bits (32),  Expect = 1.8
  Identities = 22/26 (85%), Gaps = 0/26 (0%)
  Strand=Plus/Plus
Query  662      TGGTGGTATTGTAGCTATCGTAGTAA  687
          |||
Sbjct  1077771  TGGTGGTATTGTTGGTATTGTAGAAA  1077796

```

3.1.476 NC_045512.2 SARS-Cov-2 1116-1133:

TTCAACCAAGGGTTGAAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1116-1133
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 366      TTCAACCAAGGGTTGAAA 383
          |||
Sbjct 1356270  TTCAACCAAGGGTTGCAA 1356287
```

3.1.477 NC_045512.2 SARS-Cov-2 7192-7219:

TACCATTTTCATCTTTTAAATGGGATTTA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7192-7219
Score = 29.2 bits (31), Expect = 6.2
Identities = 23/28 (82%), Gaps = 0/28 (0%)
Strand=Plus/Minus
Query 442      TACCATTTTCATCTTTTAAATGGGATTTA 469
          || |||
Sbjct 1288375  TAACATTTTCATCTTATATAGGTGATTTA 1288348
```

3.1.478 NC_045512.2 SARS-Cov-2 12170-12207:

GCTAATGGTGATTCTGAAGTTGTTCTTAAAAAGTTGAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12170-12207
Score = 31.9 bits (34), Expect = 0.51
Identities = 30/38 (79%), Gaps = 3/38 (8%)
Strand=Plus/Minus
Query 420      GCTAATGGTGATTCTGAAGTTGTTCTTAAAAAGTTGAA 457
          ||| ||| |||
Sbjct 1289682  GCTAATGTTG---CTGAGGGTGTCTTAAAAAGTTGAA 1289648
```

3.1.479 NC_045512.2 SARS-Cov-2 6333-6348:

ATTCGTTTGTACT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 6333-6348
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 583      ATTCGTTTGATGTACT 598
          |||
Sbjct 946141  ATTCGTTTGATGTACT 946126

```

3.1.480 NC_045512.2 SARS-Cov-2 23799-23816:

CAACTGAATGCAGCAATC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23799-23816
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 49      CAACTGAATGCAGCAATC 66
          |||
Sbjct 769165  CAACTGTATGCAGCAATC 769182

```

3.1.481 NC_045512.2 SARS-Cov-2 2884-2903:

TGTTGTGGCAGATGCTGTCA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2884-2903
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 134     TGTTGTGGCAGATGCTGTCA 153
          |||
Sbjct 70691   TGTTGTGGCAGATGGTTTCA 70710

```

3.1.482 NC_045512.2 SARS-Cov-2 29722-29735:

CACATTTTCACCGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29722-29735
Score = 26.5 bits (28), Expect = 9.5
Identities = 14/14 (100%), Gaps = 0/14 (0%)

```

```

Strand=Plus/Plus
Query 272      CACATTTTCACCGA 285
          |||||
Sbjct 1977460  CACATTTTCACCGA 1977473

```

3.1.483 NC_045512.2 SARS-Cov-2 2345-2360:

ATTATTGGTGGAGCTA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2345-2360
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 595      ATTATTGGTGGAGCTA 610
          |||||
Sbjct 1738631  ATTATTGGTGGAGCTA 1738616

```

3.1.484 NC_045512.2 SARS-Cov-2 17349-17370:

TGTCTTTGATGAAATTTCAATG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17349-17370
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/22 (91%), Gaps = 2/22 (9%)
Strand=Plus/Plus
Query 599      TGTCTTTGATGAAATTTCAATG 620
          |||||
Sbjct 889896   TGTCTTTGATGAAA--TCAATG 889915

```

3.1.485 NC_045512.2 SARS-Cov-2 20629-20653:

CATGTAGAAACATTTTACCCAAAAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 20629-20653
Score = 28.3 bits (30), Expect = 6.2
Identities = 21/25 (84%), Gaps = 0/25 (0%)
Strand=Plus/Plus
Query 879      CATGTAGAAACATTTTACCCAAAAT 903
          ||| || |||||
Sbjct 2146343  CATCTAAAACATTTTACAAAAAAT 2146367

```

3.1.486 NC_045512.2 SARS-Cov-2 17385-17400:

TTTGAGTGTTCAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17385-17400
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 635      TTTGAGTGTTCAT 650
          |||
Sbjct 1550969  TTTGAGTGTTCAT 1550954
```

3.1.487 NC_045512.2 SARS-Cov-2 3668-3683:

TATGAAAATTTAATC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3668-3683
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 918      TATGAAAATTTAATC 933
          |||
Sbjct 1468174  TATGAAAATTTAATC 1468159
```

3.1.488 NC_045512.2 SARS-Cov-2 29550-29563:

CAAGGCAGATGGGC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29550-29563
Score = 26.5 bits (28), Expect = 9.5
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Plus
Query 100      CAAGGCAGATGGGC 113
          |||
Sbjct 605674  CAAGGCAGATGGGC 605687
```

3.1.489 NC_045512.2 SARS-Cov-2 5962-5984:

TTATAAGAAAGACAATTCTTATT

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 5962-5984
 Score = 33.7 bits (36), Expect = 0.15
 Identities = 21/23 (91%), Gaps = 0/23 (0%)
 Strand=Plus/Plus
 Query 212 TTATAAGAAAGACAATTCTTATT 234
 ||||| |||||||
 Sbjct 859158 TTATAAGATGGACAATTCTTATT 859180

3.1.490 NC_045512.2 SARS-Cov-2 7919-7933:

TCATCTGCAAAATCA

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 7919-7933
 Score = 28.3 bits (30), Expect = 6.2
 Identities = 15/15 (100%), Gaps = 0/15 (0%)
 Strand=Plus/Plus
 Query 169 TCATCTGCAAAATCA 183
 |||||
 Sbjct 1501868 TCATCTGCAAAATCA 1501882

3.1.491 NC_045512.2 SARS-Cov-2 21951-22005:

TCTGTGAATTTCAATTTTGTAATGATCCATTTTGGGTGTTTATTACCACAAAAA

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 21947-22005
 Score = 33.7 bits (36), Expect = 0.15
 Identities = 44/59 (75%), Gaps = 3/59 (5%)
 Strand=Plus/Minus
 Query 197 AAAGTCTGTGAATTTCAATTTTGTAATGATCCATTTTGGGTGTTTATTACCACAAAAA 255
 ||| ||| || ||| |||| | | ||| | | ||| ||||| | ||||
 Sbjct 1705768 AAATTCTATGCATTTGGATTTTCTGA--ATCGAATGTTGG-TGTTTATTACAATAAAAA 170571

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 21951-22005
 Score = 31.0 bits (33), Expect = 1.8
 Identities = 41/55 (75%), Gaps = 3/55 (5%)
 Strand=Plus/Minus
 Query 1 TCTGTGAATTTCAATTTTGTAATGATCCATTTTGGGTGTTTATTACCACAAAAA 55
 ||| || |||| |||| | | ||| | | ||| ||||| | ||||

Sbjct 1705764 TCTATGCATTGGATTTCTGA--ATCGAATGTTGG-TGTTTATTACAATAAAAA 1705713

3.1.492 NC_045512.2 SARS-Cov-2 21999-22013:

ACAAAAACAACAAAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 21999-22013
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 249      AAAAAACAACAAAA 263
          |||
Sbjct 1148897  AAAAAACAACAAAA 1148883
```

3.1.493 NC_045512.2 SARS-Cov-2 20947-20969:

GATTCAGATCTTAATGACTTTGT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 20947-20969
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/23 (87%), Gaps = 0/23 (0%)
Strand=Plus/Plus
Query 197      GATTCAGATCTTAATGACTTTGT 219
          ||| |||| | |||
Sbjct 834802   GATGCAGATATCAATGACTTTGT 834824
```

3.1.494 NC_045512.2 SARS-Cov-2 10027-10050:

AACCTCT---ATCACCTCAGCTGTTTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 10027-10050
Score = 30.1 bits (32), Expect = 1.8
Identities = 23/27 (85%), Gaps = 3/27 (11%)
Strand=Plus/Plus
Query 277      AACCTCT---ATCACCTCAGCTGTTTT 300
          ||| ||| |||
Sbjct 1479078   AACCTCGCCATCAACTCAGCTGTTTT 1479104
```

3.1.495 NC_045512.2 SARS-Cov-2 575-592:

CTTGGTGTCCCTTGTCCCT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 575-592
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 125      CTTGGTGTCCCTTGTCCCT 142
          ||||| |||||
Sbjct 1788767 CTTGGTATCCTTGTCCCT 1788750
```

3.1.496 NC_045512.2 SARS-Cov-2 20876-20905:

GTTCTGATAAAGGAGTTGCACCAGGTACAG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 20876-20905
Score = 32.8 bits (35), Expect = 0.51
Identities = 25/30 (83%), Gaps = 0/30 (0%)
Strand=Plus/Plus
Query 126      GTTCTGATAAAGGAGTTGCACCAGGTACAG 155
          || ||||| ||||| |||| | ||||
Sbjct 988422    GTGCTGATAAAGGAGTTTACCATGGACAG 988451
```

3.1.497 NC_045512.2 SARS-Cov-2 23166-23194:

AAAACAAATGTGT-CAATTTCAACTTCAAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23166-23194
Score = 30.1 bits (32), Expect = 1.8
Identities = 26/30 (87%), Gaps = 2/30 (7%)
Strand=Plus/Minus
Query 416      AAAACAAATGTGT-CAATTTCAACTTCAAT 444
          ||| |||| |||| | |||||
Sbjct 700818    AAATCAAA-GTGTACTATTTCAACTTCAAT 700790
```

3.1.498 NC_045512.2 SARS-Cov-2 21188-21203:

ATGCTGATCTTTATAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 21188-21203
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus
Query 438      ATGCTGATCTTTATAA 453
          |||
Sbjct 1060251  ATGCTGATCTTTATAA 1060266

```

3.1.499 NC_045512.2 SARS-Cov-2 3188-3202:

CAAGAAGAAGATTGG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3188-3202
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 438      CAAGAAGAAGATTGG 452
          |||
Sbjct 377976   CAAGAAGAAGATTGG 377990

```

3.1.500 NC_045512.2 SARS-Cov-2 22282-22299:

TTTACTTGCTTTACATAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22282-22299
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 532      TTTACTTGCTTTACATAG 549
          |||
Sbjct 60014   TTTACTTGCTTTACAGAG 60031

```

3.1.501 NC_045512.2 SARS-Cov-2 9784-9798:

TACTTTTGAAGAAGC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 9784-9798
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)

```

Strand=Plus/Minus
Query 34 TACTTTTGAAGAAGC 48
|||||
Sbjct 961524 TACTTTTGAAGAAGC 961510

3.1.502 NC_045512.2 SARS-Cov-2 4192-4211:

TACTGAAATGCTAGCGAAAG

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4192-4211
Score = 32.8 bits (35), Expect = 0.51
Identities = 19/20 (95%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 442 TACTGAAATGCTAGCGAAAG 461
|||||
Sbjct 543439 TACTGAAATGCTTGCAGAAAG 543458

3.1.503 NC_045512.2 SARS-Cov-2 20876-20898:

GTTCTGATAAAGGAGTTGCACCA

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 20876-20898
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/23 (87%), Gaps = 0/23 (0%)
Strand=Plus/Plus
Query 976 GTTCTGATAAAGGAGTTGCACCA 998
|| |||||
Sbjct 988422 GTGCTGATAAAGGAGTTTTACCA 988444

3.1.504 NC_045512.2 SARS-Cov-2 24789-24803:

CAACTGCTCCTGCCA

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 24789-24803
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 39 CAACTGCTCCTGCCA 53
|||||
Sbjct 829404 CAACTGCTCCTGCCA 829390

3.1.505 NC_045512.2 SARS-Cov-2 16312-16326:

TGTTGTAAATGCTGT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 16312-16326
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 562      TGTTGTAAATGCTGT 576
          |||
Sbjct 761877   TGTTGTAAATGCTGT 761863
```

3.1.506 NC_045512.2 SARS-Cov-2 3393-3417:

CAGACATTGTGGAAGAAGCTAAAAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3393-3417
Score = 32.8 bits (35), Expect = 0.51
Identities = 22/25 (88%), Gaps = 0/25 (0%)
Strand=Plus/Minus
Query 643      CAGACATTGTGGAAGAAGCTAAAAA 667
          || ||| |||
Sbjct 1462718  CAAACATTGAAGAAGAAGCTAAAAA 1462694
```

3.1.507 NC_045512.2 SARS-Cov-2 10137-10160:

ACGGTCTTTGGCTTGATGACGTAG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 10137-10160
Score = 35.6 bits (38), Expect = 0.042
Identities = 22/24 (92%), Gaps = 0/24 (0%)
Strand=Plus/Minus
Query 387      ACGGTCTTTGGCTTGATGACGTAG 410
          ||| |||
Sbjct 435478   ACGGTCATTGGCTTGATGAAGTAG 435455
```

3.1.508 NC_045512.2 SARS-Cov-2 29704-29717:

AGGACTTGAAAGAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29698-29717
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 948      TTAGGGAGGACTTGAAAGAG 967
          ||| | |||
Sbjct 1129481  TTATGAAGGACTTGAAAGAG 1129462

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29704-29717
Score = 26.5 bits (28), Expect = 4.0
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Minus
Query 4        AGGACTTGAAAGAG 17
          |||
Sbjct 1129475  AGGACTTGAAAGAG 1129462

```

3.1.509 NC_045512.2 SARS-Cov-2 28224-28242:

TATCATGACGTTTCGTGTTG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 28224-28242
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Plus
Query 474      TATCATGACGTTTCGTGTTG 492
          |||
Sbjct 1233387  TATCATGGCGTTTCGTGTTG 1233405

```

3.1.510 NC_045512.2 SARS-Cov-2 4782-4802:

CACTTGCTGGTTCCTATAAAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4782-4802
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 32       CACTTGCTGGTTCCTATAAAG 52
          |||

```

Sbjct 1528244 CACTTGCTGGTTCCTGCAAAG 1528264

3.1.511 NC_045512.2 SARS-Cov-2 23142-23160:

CTAA-AAAGTCTACTAATTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 23142-23160
Score = 29.2 bits (31), Expect = 6.2
Identities = 19/20 (95%), Gaps = 1/20 (5%)
Strand=Plus/Plus
Query 392      CTAA-AAAGTCTACTAATTT 410
          |||| |
Sbjct 1714345  CTAAGAAAGTCTACTAATTT 1714364
```

3.1.512 NC_045512.2 SARS-Cov-2 29432-29446:

AAGAAACAGCAAACCT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29432-29446
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 682      AAGAAACAGCAAACCT 696
          ||
Sbjct 1839442  AAGAAACAGCAAACCT 1839456
```

3.1.513 NC_045512.2 SARS-Cov-2 6311-6325:

ACAAAACCAGTTGAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 6311-6325
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 561      ACAAAAACCAGTTGAA 575
          ||
Sbjct 663710  ACAAAAACCAGTTGAA 663724
```

3.1.514 NC_045512.2 SARS-Cov-2 11987-12006:

TTTGAAAAAATGGTTTCACT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11987-12006
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 237      TTTGAAAAAATGGTTTCACT 256
      |||| |
Sbjct 1687849  TTTGGAAAAAATGGTTTGA 1687868
```

3.1.515 NC_045512.2 SARS-Cov-2 24487-24501:

TGTTTTAAATGATAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 24487-24501
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 737      TGTTTTAAATGATAT 751
      ||
Sbjct 1052823  TGTTTTAAATGATAT 1052837
```

3.1.516 NC_045512.2 SARS-Cov-2 2220-2234:

TCTCAACCTGTGCTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2220-2234
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 470      TCTCAACCTGTGCTT 484
      ||
Sbjct 454230  TCTCAACCTGTGCTT 454216
```

3.1.517 NC_045512.2 SARS-Cov-2 4734-4751:

TTACTTCTTCTTCTAAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4734-4751
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 934      TTACTTCTTCTTCTAAAA 951
          |||
Sbjct 969957  TTACTTCTTCTTTAAAA 969940

```

3.1.518 NC_045512.2 SARS-Cov-2 13207-13221:

CAATATGGATCAAGA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13207-13221
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 457      CAATATGGATCAAGA 471
          |||
Sbjct 1072160  CAATATGGATCAAGA 1072174

```

3.1.519 NC_045512.2 SARS-Cov-2 13540-13557:

GCTTTTGACATCTACAAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13540-13557
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 790      GCTTTTGACATCTACAAT 807
          |||
Sbjct 1709863  GCTTTTGACATATAACAAT 1709846

```

3.1.520 NC_045512.2 SARS-Cov-2 13085-13109:

GTAGATGCTGCTAAAGCTTACAAAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13085-13109
Score = 28.3 bits (30), Expect = 6.2
Identities = 21/25 (84%), Gaps = 0/25 (0%)

```

```

Strand=Plus/Plus
Query 335      GTAGATGCTGCTAAAGCTTACAAAG 359
          ||||| ||||| ||||| || |||||
Sbjct 2120013  GTAGGTGCTGCTAAAGGGTATAAAG 2120037

```

3.1.521 NC_045512.2 SARS-Cov-2 7247-7264:

TTTTTGGCATATATTCTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7247-7264
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 497      TTTTTGGCATATATTCTT 514
          ||||| ||||| |||||
Sbjct 2065685  TTTTGGCCATATATTCTT 2065702

```

3.1.522 NC_045512.2 SARS-Cov-2 17379-17416:

TTATGATTTGAGTGTTGTCAATGCCAGATTACGTGCTA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17379-17416
Score = 30.1 bits (32), Expect = 1.8
Identities = 30/38 (79%), Gaps = 1/38 (3%)
Strand=Plus/Plus
Query 629      TTATGATTTGAGTGTTGTCAATGCCAGATTACGTGCTA 666
          ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 544290  TTATGATTTGAGTGAT-CCAAGGTCAAATAAGTGCTA 544326

```

3.1.523 NC_045512.2 SARS-Cov-2 7537-7554:

AACTATTGTTAATGGTGT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7537-7554
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 787      AACTATTGTTAATGGTGT 804
          ||| ||||| ||||| |||||
Sbjct 1370704  AACCATTGTTAATGGTGT 1370687

```

3.1.524 NC_045512.2 SARS-Cov-2 1352-1369:

AATGCTGTTGTAAAATT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1352-1369
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 602      AATGCTGTTGTAAAATT 619
          || |||
Sbjct 1277306  AAGGCTGTTGTAAAATT 1277323
```

3.1.525 NC_045512.2 SARS-Cov-2 6871-6922:

TGTTAAGAGTGTTCGGTA——AATTTTGTCTAGAGGCTTCATTTAATTATTTGAAG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 6871-6922
Score = 35.6 bits (38), Expect = 0.042
Identities = 43/60 (72%), Gaps = 8/60 (13%)
Strand=Plus/Plus
Query 121      TGTTAAGAGTGTTCGGTA-----AATTTTGTCTAGAGGCTTCATTTAATTATTTGAAG 172
          ||||| |||
Sbjct 486268  TGTTACGAGTGTCTGTATTGGAAAAATTTTGTCTATAGAATTCTTTAAATGATATGAAG 486327
```

3.1.526 NC_045512.2 SARS-Cov-2 7590-7607:

AAGGCTTTTGCAAACACTAC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7590-7607
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 840      AAGGCTTTTGCAAACACTAC 857
          |||||
Sbjct 589198  AAGGCTTTTGCTAACTAC 589215
```

3.1.527 NC_045512.2 SARS-Cov-2 1785-1804:

GTAATTTTAAAGTTACAAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1785-1804
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 35          GTAATTTTAAAGTTACAAAA 54
          ||| | | | | | | | | | | | | | |
Sbjct 1382620    GTAATTTTAAACTAACAAAA 1382601

```

3.1.528 NC_045512.2 SARS-Cov-2 29812-29824:

AAAATTAATTTTA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29812-29824
Score = 24.7 bits (26), Expect = 6.3
Identities = 13/13 (100%), Gaps = 0/13 (0%)
Strand=Plus/Plus
Query 12          AAAATTAATTTTA 24
          ||| | | | | | | | | |
Sbjct 1731924    AAAATTAATTTTA 1731936

```

3.1.529 NC_045512.2 SARS-Cov-2 19697-19716:

TCATTAATAACACTGTTTAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19697-19716
Score = 32.8 bits (35), Expect = 0.51
Identities = 19/20 (95%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 947          TCATTAATAACACTGTTTAC 966
          || ||| | | | | | | | | | | | | |
Sbjct 1150549    TCGTTAATAACACTGTTTAC 1150530

```

3.1.530 NC_045512.2 SARS-Cov-2 14843-14874:

AACTACTATTTGTAGTTGAAGTTGTTGATAAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 14843-14874
Score = 29.2 bits (31), Expect = 6.2
Identities = 26/32 (81%), Gaps = 2/32 (6%)

```

```

Strand=Plus/Minus
Query 93      AACTACTATTTGTAGTTGAAGTTGTTGATAAG 124
            ||| || |||||  ||||| |||||
Sbjct 1570829 AACACAATTTGC--TTGAAATTGTTGATAAG 1570800

```

3.1.531 NC_045512.2 SARS-Cov-2 20975-20989:

ATGCAGATTCAACTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 20975-20989
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 225      ATGCAGATTCAACTT 239
            |||||
Sbjct 326457   ATGCAGATTCAACTT 326443

```

3.1.532 NC_045512.2 SARS-Cov-2 14075-14090:

TCAATGGTAACTGGTA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 14075-14090
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus
Query 325      TCAATGGTAACTGGTA 340
            |||||
Sbjct 411003   TCAATGGTAACTGGTA 411018

```

3.1.533 NC_045512.2 SARS-Cov-2 22491-22510:

AAGGAATCTATCAAACCTTCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22491-22510
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 741      AAGGAATCTATCAAACCTTCT 760
            || ||| |||||
Sbjct 1240174   AATGAACTATCAAACCTTCT 1240193

```

3.1.534 NC_045512.2 SARS-Cov-2 4360-4374:

AGAAATTCTTGGAAC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4352-4374
Score = 30.1 bits (32), Expect = 1.8
Identities = 21/23 (91%), Gaps = 1/23 (4%)
Strand=Plus/Plus
Query 602      GAGAAGCAAGAAATTCTTGGAAC 624
          |||
Sbjct 190189   GAGAAGCAAGAAA-TCGTGGAAC 190210
```

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4360-4374
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 610      AGAAATTCTTGGAAC 624
          |||
Sbjct 64390   AGAAATTCTTGGAAC 64404
```

3.1.535 NC_045512.2 SARS-Cov-2 1123-1147:

AAGGGTTGAAAAGAAAAAGCTTGAT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 1123-1147
Score = 28.3 bits (30), Expect = 6.2
Identities = 21/25 (84%), Gaps = 0/25 (0%)
Strand=Plus/Plus
Query 373      AAGGGTTGAAAAGAAAAAGCTTGAT 397
          ||
Sbjct 464789   AACGGTTGAAAAGAGTAACCTTGAT 464813
```

3.1.536 NC_045512.2 SARS-Cov-2 25744-25765:

ATAAACTTTGTAAGAATAATAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 25744-25765
Score = 28.3 bits (30), Expect = 6.2
```

Identities = 20/22 (91%), Gaps = 1/22 (5%)
 Strand=Plus/Plus
 Query 944 ATAAACTTTGTAAGAATAATAA 965
 ||||| ||| |||||
 Sbjct 522809 ATAAATTTT-TAAGAATAATAA 522829

3.1.537 NC_045512.2 SARS-Cov-2 14049-14066:

TGTACTGACATTAGATAA

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 14049-14066
 Score = 29.2 bits (31), Expect = 6.2
 Identities = 17/18 (94%), Gaps = 0/18 (0%)
 Strand=Plus/Minus
 Query 299 TGTACTGACATTAGATAA 316
 ||||| |||||
 Sbjct 2147245 TGTACTCACATTAGATAA 2147228

3.1.538 NC_045512.2 SARS-Cov-2 23711-23732:

AATTTTACTATTAGTGTTACCA

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 23711-23732
 Score = 31.9 bits (34), Expect = 0.51
 Identities = 20/22 (91%), Gaps = 0/22 (0%)
 Strand=Plus/Minus
 Query 961 AATTTTACTATTAGTGTTACCA 982
 ||||| ||||| ||| |||||
 Sbjct 543686 AATTTTACTATAAGTCTTACCA 543665

3.1.539 NC_045512.2 SARS-Cov-2 27750-27778:

GACAGAATGATTGAACTTTCATTAATTGA

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
 Length=2148350
 Query = NC_045512.2 SARS-Cov-2 27750-27778
 Score = 31.0 bits (33), Expect = 1.8
 Identities = 24/29 (83%), Gaps = 0/29 (0%)
 Strand=Plus/Minus
 Query 950 GACAGAATGATTGAACTTTCATTAATTGA 978
 || ||||| ||||| ||| |||||
 Sbjct 1066097 GATAGAATGATTGAACTATAGTAAATTGA 1066069

3.1.540 NC_045512.2 SARS-Cov-2 15139-15154:

ACCAATAGACAGTTTC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15139-15154
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus
Query 389      ACCAATAGACAGTTTC 404
          |||
Sbjct 2059879  ACCAATAGACAGTTTC 2059894
```

3.1.541 NC_045512.2 SARS-Cov-2 22314-22334:

CTGGTGATTCTTCTTCAGGTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22314-22334
Score = 34.6 bits (37), Expect = 0.15
Identities = 20/21 (95%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 564      CTGGTGATTCTTCTTCAGGTT 584
          |||
Sbjct 1139623  CTGGTGATTCTTCTTCAGGTT 1139643
```

3.1.542 NC_045512.2 SARS-Cov-2 19701-19716:

TAATAACACTGTTTAC

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19697-19716
Score = 32.8 bits (35), Expect = 0.51
Identities = 19/20 (95%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 947      TCATTAATAACACTGTTTAC 966
          ||
Sbjct 1150549  TCGTTAATAACACTGTTTAC 1150530
```

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 19701-19716
Score = 30.1 bits (32), Expect = 1.8
```

Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 1 TAATAAACTGTTTAC 16
|||||
Sbjct 1150545 TAATAAACTGTTTAC 1150530

3.1.543 NC_045512.2 SARS-Cov-2 6110-6129:

AAACCTGCTTCAAGAGAGCT

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 6110-6129
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 360 AAACCTGCTTCAAGAGAGCT 379
||| |||||
Sbjct 787435 AAATCTGCTTCAAGAGACCT 787454

3.1.544 NC_045512.2 SARS-Cov-2 20255-20270:

ATTTCTTAGAATTAGC

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 20255-20270
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus
Query 505 ATTTCTTAGAATTAGC 520
|||||
Sbjct 1439588 ATTTCTTAGAATTAGC 1439603

3.1.545 NC_045512.2 SARS-Cov-2 21404-21423:

AATTTCCCCTTAAATTAAGG

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 21404-21423
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 654 AATTTCCCCTTAAATTAAGG 673
||||| || |||||
Sbjct 681016 AATTTCCCCTTAAAGTAAGG 681035

3.1.546 NC_045512.2 SARS-Cov-2 7338-7352:

TTATTAGTAATTCTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 7338-7352
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 588      TTATTAGTAATTCTT 602
          |||
Sbjct 580564  TTATTAGTAATTCTT 580550
```

3.1.547 NC_045512.2 SARS-Cov-2 10409-10431:

AATGGTTCACCATCTGGTGTTTA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 10409-10431
Score = 29.2 bits (31), Expect = 6.2
Identities = 20/23 (87%), Gaps = 0/23 (0%)
Strand=Plus/Minus
Query 659      AATGGTTCACCATCTGGTGTTTA 681
          |||
Sbjct 519445  AATGGTTCACCTTCTGTTGTATA 519423
```

3.1.548 NC_045512.2 SARS-Cov-2 27898-27913:

AATTTCTTGTTTTCTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 27898-27913
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus
Query 148      AATTTCTTGTTTTCTT 163
          |||
Sbjct 1157056  AATTTCTTGTTTTCTT 1157071
```

3.1.549 NC_045512.2 SARS-Cov-2 29468-29481:

GATTTGGATGATTT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29468-29481
Score = 26.5 bits (28), Expect = 9.5
Identities = 14/14 (100%), Gaps = 0/14 (0%)
Strand=Plus/Minus
Query 18      GATTTGGATGATTT 31
          |||
Sbjct 582537  GATTTGGATGATTT 582524

```

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 29463-29481
Score = 26.5 bits (28), Expect = 9.5
Identities = 17/19 (89%), Gaps = 0/19 (0%)
Strand=Plus/Minus
Query 13      CTGCAGATTTGGATGATTT 31
          ||| |||
Sbjct 1156350  CTGAAGATTTGGATGAATT 1156332

```

3.1.550 NC_045512.2 SARS-Cov-2 27309-27326:

AATTAAAAATTTATCTAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 27309-27326
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 559     AATTAAAAATTTATCTAA 576
          || |||
Sbjct 307210  AACTAAAAATTTATCTAA 307193

```

3.1.551 NC_045512.2 SARS-Cov-2 28850-28867:

AGTTCAAGAAATTCAACT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 28850-28867
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 100     AGTTCAAGAAATTCAACT 117
          ||| |||

```

Sbjct 705563 AGTTCAAGAAATTGAACT 705546

3.1.552 NC_045512.2 SARS-Cov-2 3076-3090:

AGAAGAAGAGTTTGA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3076-3090
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 326 AGAAGAAGAGTTTGA 340
      |||
Sbjct 25512 AGAAGAAGAGTTTGA 25498
```

3.1.553 NC_045512.2 SARS-Cov-2 12707-12725:

GCACTACGACAGATGTCTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 12707-12725
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Plus
Query 957 GCACTACGACAGATGTCTT 975
      |||
Sbjct 1459252 GCACTACGACAGATTCTT 1459270
```

3.1.554 NC_045512.2 SARS-Cov-2 15972-15987:

AGATGATATCGTAAAA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15972-15987
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Minus
Query 222 AGATGATATCGTAAAA 237
      |||
Sbjct 1673314 AGATGATATCGTAAAA 1673299
```

3.1.555 NC_045512.2 SARS-Cov-2 22802-22819:

CAAACCTGGAAAGATTGCT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22802-22819
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 52          CAAACCTGGAAAGATTGCT 69
          ||||| |||||
Sbjct 1455761    CAAACCGGAAAGATTGCT 1455778
```

3.1.556 NC_045512.2 SARS-Cov-2 11129-11146:

TCTGCTTTTGCAATGATG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11129-11146
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Minus
Query 379        TCTGCTTTTGCAATGATG 396
          |||||
Sbjct 260394    TCTGCTTTTGCAATTATG 260377
```

3.1.557 NC_045512.2 SARS-Cov-2 17086-17100:

CCTGGTACTGGTAAG

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17086-17100
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 986        CCTGGTACTGGTAAG 1000
          |||||
Sbjct 420220    CCTGGTACTGGTAAG 420206
```

3.1.558 NC_045512.2 SARS-Cov-2 10737-10756:

ATGACTTTAACCTTGTGGCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 10737-10756
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query 937      ATGACTTTAACCTTGTGGCT 956
          |||
Sbjct 1056512 ATGACTTTAACCTGGTGACT 1056531

```

3.1.559 NC_045512.2 SARS-Cov-2 5815-5829:

TGCTTTACTTACAAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 5815-5829
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 65      TGCTTTACTTACAAA 79
          |||
Sbjct 880384  TGCTTTACTTACAAA 880370

```

3.1.560 NC_045512.2 SARS-Cov-2 3851-3865:

GAAAAGCAAGTTGAA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3851-3865
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 101     GAAAAGCAAGTTGAA 115
          |||
Sbjct 1051300 GAAAAGCAAGTTGAA 1051314

```

3.1.561 NC_045512.2 SARS-Cov-2 21464-21487:

ATATGATTTTATCTCTTCTTAGTA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 21464-21487
Score = 31.0 bits (33), Expect = 1.8
Identities = 21/24 (88%), Gaps = 0/24 (0%)

```

```

Strand=Plus/Minus
Query 714      ATATGATTTTATCTCTTCTTAGTA 737
          ||||  ||||  |||||
Sbjct 530816   ATATATTTTTGTCTCTTCTTAGTA 530793

```

3.1.562 NC_045512.2 SARS-Cov-2 3029-3049:

TGTTCTTTCTACCCTCCAGAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3029-3049
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 279      TGTTCTTTCTACCCTCCAGAT 299
          |||||
Sbjct 994273   TGTTCTTTCTACACTTCAGAT 994293

```

3.1.563 NC_045512.2 SARS-Cov-2 13681-13701:

CAACATGAAGAAACAATTTAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 13681-13701
Score = 30.1 bits (32), Expect = 1.8
Identities = 19/21 (90%), Gaps = 0/21 (0%)
Strand=Plus/Plus
Query 931      CAACATGAAGAAACAATTTAT 951
          || |||||
Sbjct 2131483  CATCATGAAAAACAATTTAT 2131503

```

3.1.564 NC_045512.2 SARS-Cov-2 3804-3818:

AAAATCTCTATGACA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 3804-3818
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 54      AAAATCTCTATGACA 68
          |||||
Sbjct 1612147  AAAATCTCTATGACA 1612133

```

3.1.565 NC_045512.2 SARS-Cov-2 15644-15663:

GAGATGTTGACACAGACTTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 15644-15663
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Minus
Query 894      GAGATGTTGACACAGACTTT 913
          ||| | | | | | | | | | | | | | | |
Sbjct 1361161 GAGATGTTGACTCAGAATTT 1361142
```

3.1.566 NC_045512.2 SARS-Cov-2 16963-16980:

CAAGAGCACTATGTTAGA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 16963-16980
Score = 29.2 bits (31), Expect = 6.2
Identities = 17/18 (94%), Gaps = 0/18 (0%)
Strand=Plus/Plus
Query 213      CAAGAGCACTATGTTAGA 230
          ||| | | | | | | | | | | |
Sbjct 749733 CAAGATCACTATGTTAGA 749750
```

3.1.567 NC_045512.2 SARS-Cov-2 4754-4768:

CCTGAAGAACATTTT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4754-4768
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 4        CCTGAAGAACATTTT 18
          ||| | | | | | | | | | | |
Sbjct 1702951 CCTGAAGAACATTTT 1702937
```

3.1.568 NC_045512.2 SARS-Cov-2 4782-4796:

CACTTGCTGGTTCCT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4782-4796
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 982      CACTTGCTGGTTCCT 996
          |||
Sbjct 1528244 CACTTGCTGGTTCCT 1528258

```

3.1.569 NC_045512.2 SARS-Cov-2 2809-2833:

GATTGATAAAGTACTTAATGAGAAG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 2809-2833
Score = 28.3 bits (30), Expect = 6.2
Identities = 21/25 (84%), Gaps = 0/25 (0%)
Strand=Plus/Minus
Query 59      GATTGATAAAGTACTTAATGAGAAG 83
          |||
Sbjct 1665811 GATTGATAAAGAAGTTTCTGAAAAG 1665787

```

3.1.570 NC_045512.2 SARS-Cov-2 5555-5570:

GGTGTAGAAGCTGTTA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 5555-5570
Score = 30.1 bits (32), Expect = 1.8
Identities = 16/16 (100%), Gaps = 0/16 (0%)
Strand=Plus/Plus
Query 805      GGTGTAGAAGCTGTTA 820
          |||
Sbjct 1711183 GGTGTAGAAGCTGTTA 1711198

```

3.1.571 NC_045512.2 SARS-Cov-2 16603-16641:

GCTAACACCTGTACTGAAAGACTCAAGCTTTTTGCAGCA

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 16603-16641
Score = 29.2 bits (31), Expect = 6.2
Identities = 30/39 (77%), Gaps = 3/39 (8%)

```

```

Strand=Plus/Plus
Query  853      GCTAACACCTGTAAGACTCAAGCTTTTTGCAGCA  891
          ||||  |||  ||  |||||  |||||  ||||  |||||
Sbjct  1129748  GCTACAACCAGTTCTGAAAGACTCA---TTTTCTCAGCA  1129783

```

3.1.572 NC_045512.2 SARS-Cov-2 26086-26104:

ATCTACAATAAAATTGTTG

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 26086-26104
Score = 31.0 bits (33), Expect = 1.8
Identities = 18/19 (95%), Gaps = 0/19 (0%)
Strand=Plus/Minus
Query  336      ATCTACAATAAAATTGTTG  354
          ||||  |||||  |||||  |||||
Sbjct  41030  ATCTAGAATAAAATTGTTG  41012

```

3.1.573 NC_045512.2 SARS-Cov-2 22890-22909:

CTAAGGTTGGTGGTAATTAT

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 22890-22909
Score = 28.3 bits (30), Expect = 6.2
Identities = 18/20 (90%), Gaps = 0/20 (0%)
Strand=Plus/Plus
Query  140      CTAAGGTTGGTGGTAATTAT  159
          |||||  |||||  ||  |||
Sbjct  830301  CTAAGGTTGGTGAAACTAT  830320

```

3.1.574 NC_045512.2 SARS-Cov-2 4740-4754:

CTTCTTCTAAAACAC

```

> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 4740-4754
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query  940      CTTCTTCTAAAACAC  954
          |||||  |||||  |||||
Sbjct  1928562  CTTCTTCTAAAACAC  1928576

```

3.1.575 NC_045512.2 SARS-Cov-2 11174-11188:

TGTTTGT TTTTGTTA

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 11174-11188
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Plus
Query 424      TGTTTGT TTTTGTTA 438
          |||
Sbjct 1158047 TGTTTGT TTTTGTTA 1158061
```

3.1.576 NC_045512.2 SARS-Cov-2 17436-17450:

CGACCCTGCTCAATT

```
> NZ_CP020549.1 Streptococcus pneumoniae strain Hu17 chromosome
Length=2148350
Query = NC_045512.2 SARS-Cov-2 17436-17450
Score = 28.3 bits (30), Expect = 6.2
Identities = 15/15 (100%), Gaps = 0/15 (0%)
Strand=Plus/Minus
Query 986      CGACCCTGCTCAATT 1000
          |||
Sbjct 1323958 CGACCCTGCTCAATT 1323944
```